```
(without alignments)
297.593 Million cell updates/sec
                                                                                                                 2002, 09:59:15 ; Search time 72.0896 Seconds
                                                                                                                                                                                                                                    1 DSEEDEEHTIITDTELPPLK.......ECKNICEDGPNGFQVDNYGT 161
                                                                                                                                                                                                                                                                                                                                                                          908470
                        Compugen Ltd.
GenCore version 5.1.3
Copyright (c) 1993 - 2002 Compuc
                                                                                                                                                                                                                                                                                                                                                                        Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                    908470 seqs, 133250620 residues
                                                                               OM protein - protein search, using sw model
                                                                                                                                                                                                                                                                           BLOSUM62
Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                                                                                                                                                                                               Minimum DB seq length: 0
Maximum DB seq length: 200000000
                                                                                                                                                                                              US-09-741-106-19
905
                                                                                                                     'n
                                                                                                                     December
                                                                                                                                                                                                                                                                           Scoring table:
                                                                                                                                                                                                                  Perfect score:
                                                                                                                                                                                                                                        Sequence:
                                                                                                                                                                                                                                                                                                                                    Searched:
                                                                                                                     Run on:
                                                                                                                                                                                                Title:
```

Database

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result

Š.

TFPI chimeric prot TFPI mutein, Lys36 TFPI mutein K36R. Anglotensin conver Recombinant non-gl Human tissue facto Description AAR92012 AAU02971 AAW30311 AAW61535 AAR61884 AAR67994 AAY49557 AAR92011 AAW00017 a 17 117 122 128 118 116 120 DB Query Match Length 276 225 225 276 304 304 352 99 Score 8897 8897 8897 8897 8997

WO9604378-A2

15-FEB-1996

Lipoprotein-associ Tissue factor path Human lipoprotein Ubiquitin-TFPI fus

LACI fragment 1 -	Human tissue facto	Ser(Asp1-Thr255)-E	Ser-(Asp1-Glu245)-	Ser-(Asp1-Ser248)-	Ser-(Asp1-Ile253)-	_	Human lipoprotein-	Non-glycosylated T	(Aspi-Thr161)-EPI	Human mutant tissu	LAC1 gene product.	Ser-(Glu15-Thr161)	LACI. Rattus ratt	Lipoprotein-associ	r88-Th	Factor X-LACI hybr	ragment	Bovine bikunin pep	Bovine bikunin pep	Bovine bikunin pep	Synthetic yeast le	Bovine bikunin pep		Bovine bikunin pep		Bovine bikunin pep	TFPI 2. Homo sapi	Lipoprotein-associ	Human LACI-K2 doma	Human aprotinin-li	Human Kunitz-type	US5880256 Seq ID 3	Human aprotinin-li	Bovine bikunin pep
AAR23800	AAP92002	AAR11169		AAR11172	AAR11170	AAY70273	AAR78389	AAR37312	AAR11167	AAY70272	AAR42309	AAR11146	AAR35001	AAR88513	AAR11145	AAR13675	AAR23799	AAW82772	AAW82771	AAW82770	AAR39804	AAW82768	AAW82769	AAW82766	AAW82767	AAW82785	AAR39802	AAR81914	AAR78541	AAR99189	AAW64113	9	AAR99218	AAW82787
13	10	12	12	12	12	21	16	14	12	21	14	12	14	17	12	12	13	20	20	20	14	20	20	20	20	20	14	16	16	17	19	20	17	20
160	304	256	261	262	265	304	304	277	189	304	304	183	302	302	110	250	71	128	128	128	111	128	128	128	128	128	58	58	28	28	28	28	83	128
В.	ъ.	ъ.	8	ω.	8	7	97.6	7	7	9	N	-	9.59	5	47.0	47.0	45.1	41.7	41.0	0	œ	œ	37.9	~	$\sim$	7	9	ဖ	9	9	φ	Φ	36.9	36.8
892	891	890	890	890	890	886	883	881	879	876	836	825	594	594	425	425	408	377	371	370	347.5	345	343	340	337	336	334	334	334	334	334	334	334	333
11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	29	30	31	32	33	34	32	36	37	38	39	40	41	42	43	44	45

## ALIGNMENTS

```
Kunitz-type domain; C-terminal tail; tissue factor pathway inhibitor; TFPI: TFPI-2; cell surface localisation; glycosaminoglycan; heparin; phospholipid; binding; chimeric protein; mutein; substitution; Pi-reactive site; septis; septic shock; thrombosis; up-regulation; tissue factor; injury; trauma; endotoxin; TNF; cancer; IL-1; tumour necrosis factor; interleukin.
                                                                                                                                                                                                                                                                                    /note= "Second Kunitz-type domain"
Misc-difference 117
                                                                                                                                                                                                                                       26..76
/note= "First Kunitz-type domain"
                                                                                                                                                                                                                           Location/Qualifiers
                      AAW00017 standard; Protein; 161 AA.
                                                                                                                                                                                                                                                                                                                        /label= Asn117Gln
                                                                                                                                                                                                                                                                         /label= Lys36Arg
97..147
                                                                     (first entry)
                                                                                            TFPI chimeric protein.
                                                                                                                                                                                                                                                              Misc-difference
                                                                                                                                                                                                    Homo sapiens
                                                                   30-SEP-1996
                                              AAW00017;
                                                                                                                                                                                                                                      Domain
RESULT 1
           AAW00017
```

```
Domain
                                                            Domain
                                                                                         Domain
                                                                                                                        Domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAR92012
g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              δλ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      δ
                                                                                                                                                                                                                         This sequence represents a chimeric protein containing the first and second kunitz-type domain derived from tissue factor pathway inhibitor (TFPI). This sequence has a Lys to Arg mutation in the PI-reactive domain of the first Kunitz-type domain, and an Asn to Gln mutation in the PI-reactive domain of the second Kunitz-domain. The Kunitz-type domains are highly basic sequences and may be involved in cell surface localisation by glycosaminoglycan (including heparin) or phospholipid binding. Chimeric proteins such as this, having one or more substitutions exclusively in the PI-reactive site of one or more kunitz-type domains are covered within the scope of the invention. Chimeric proteins comprising the kunitz-type domains from TFPI or TFPI-2, may also comprise an alternative glycosaminoglycan binding peptide selected from those given in AAR92266-73. The chimeric proteins and muteins may be used in a pharmaceutical composition for the may be generally useful in the treatment of diseases caused by the muteins may be generally useful in the treatment of diseases caused by the muteins may be generally useful in the treatment of diseases caused by the may expenditation of tissue factor bought on by injury, trauma, endotoxin,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           61 GNQNRFESLEECKKMCTRDNANRIIKTTLQQEKPDFCFLEEDPGICRGYITRYFYNQQTK 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           61 GNONRFESLEECKKMCTRDNSNRIIKTTLQQEKPDFCFLEEDPGICRGYITRYFYUQQYK 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Kunitz-type domain; C-terminal tail; tissue factor pathway inhibitor; TFPI: TFPI-2; cell surface localisation; glycosaminoglycan; heparin; phospholipid; binding; chimeric protein; mutein; substitution; PI-reactive site; sepsis; septic shock; thrombosis; up-regulation; tissue factor; injury; trauma; endotoxin; TNF; cancer; IL-1; tumour necrosis factor; interleukin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 DSEEDEEHTIITDTELPPLKLMHSFCAFKADDGPCRAIMKRFFFNIFTRQCEFIYGGC 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 DSEEDEEHTIITDTELPPLKLMHSFCAFKADDGPCRAIMKRFFFNIFTRQCEEFIYGGCE 60
                                                                                                                                                    Chimeric protein comprising Kunitz-type domains from TFPI-1 and -2 - used for the treatment of septic shock and thrombosis disorders
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   99.7%; Score 902; DB 17; Length 161; 99.4%; Pred. No. 4.1e-83; ive 1; Mismatches 0; Indels (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      121 QCERFKYGGCLGNMNNFETLEECKNICEDGPNGFQVDNYGT 161
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      121 QCERFKYGGCLGNMNNFETLEECKNICEDGPNGFQVDNYGT 161
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TNF, cancer, IL-1 or other agents or conditions.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAR92265 standard; peptide; 276 AA.
                                                                                                                                                                                                 Claim 14; Page 19; 68pp; English
95WO-US09464
                              94US-0286521
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Matches 160; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TFPI mutein, Lys36Arg.
                                                                                        Creasey AA, Innis MA;
                                                            (CHIR ) CHIRON CORP.
                                                                                                                      WPI; 1996-129394/13.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        161 AA;
25-JUL-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         30-SEP-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Seguence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAR92265;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Key
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAR92265
à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   g
```

```
This sequence represents a mutein of tissue factor pathway inhibitor (TFPI). This sequence has a Lys to Arg mutation in the Pi-reactive domain of the first Kunitz-type domain. The Kunitz-type domains are highly basic sequences and may be involved in cell surface localisation by glycosaminoglycan (including heparin) or phospholipid binding.

Wuteins such as this, having one or more substitutions exclusively in the Pi-reactive site of one or more Kunitz-type domains are covered by the scope of the invention. Chimeric proteins comprising the kunitz-type domains from TFPI or TFP-2, may also comprise an alternative glycosaminoglycan binding peptide selected from those given in a pharmaceutical composition for the treatment of sepsis, septic shock and thrombosis disorders. The proteins may be generally useful in the treatment of diseases caused by the up-regulation of tissue factor bought on by injury, trauma, endotoxin, TNF, cancer, IL-1 or other
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  61 GNONRFESLEECKKMCTRDNANRIKTTLQQEKPDFCFLEEDPGICKGYITRYFYNNQTK 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               61 GNONRFESLEECKKMCTRDNANRIIKTTLQQEKPDFCFLEEDPGICRGYITRYFYNQQTK 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 DSEEDEEHTIITDTELPPLKLMHSFCAFKADDGPCRAIMKRFFFNIFTRQCEEFIYGGCE 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 DSEEDEEHTIITDTELPPLKLMHSFCAFKADDGPCRAIMKRFFFNIFTRQCEEFIYGGCE 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Chimeric protein comprising Kunitz-type domains from TFPI-1 and -i used for the treatment of septic shock and thrombosis disorders
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         99.4%; Score 900; DB 17; Length 276; 99.4%; Pred. No. 1.2e-82;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               121 QCERFKYGGCLGNMNNFETLEECKNICEDGPNGFQVDNYGT 161
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 121 OCERFKYGGCLGNMNNFETLEECKNICEDGPNGFQVDNYGT 161
                                                                                         97..147
/note= "Second Kunitz-type domain"
'note= "First Kunitz-type domain"
                                                                                                                                                                                             /note= "Third Kunitz-type domain"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0; Mismatches
                                                                                                                                                                                                                            240..276
/note= "C-terminal tail"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAR92012 standard; Protein; 276 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Disclosure; Page 8; 68pp; English.
                                                                 /label= Lys36Arg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           99.48;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     94US-0286521.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       95WO-US09464.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   08-MAY-1996 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Matches 160; Conservative
                                                                                                                                                                  189..239
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 1996-129394/13.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (CHIR ) CHIRON CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              276 AA;
                                     Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     05-AUG-1994;
                                                                                                                                                                                                                                                                                                                                    WO9604378-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       25-JUL-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Creasey AA,
                                                                                                                                                                                                                                                                                                                                                                                                      15-FEB-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAR92012;
```

```
WO200136632-A2
                                                                             Homo sapiens.
                                                                                                                                                                       17-NOV-1999;
                                                                                                                                                                                  10-DEC-1999;
                                                                                                                         25-MAY-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAW30311;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AX ID
g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              qq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        δλ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   δλ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Angiotensin converting enzyme splice variant; ACEV; interleukin 6; granulocyte colony stimulating factor receptor; glucagon; hypertrophy; platelet-derived endothelial cell growth factor; cardiovascular disease; cellular tumour antigen P53; cyclin-dependent kinase inhibitor 1C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            61 GNONRFESLEECKKMCTRDNANRIIKTTLQQEKPDFCFLEEDPGICRGYITRYFYNQQTK 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 DSEEDEEHTIITDTELPPLKLMHSFCAFKADDGPCRAIMKRFFFNIFTRQCEEFIYGGCE 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 DSEEDEEHTIITDTELPPLKLMHSFCAFKADDGPCRAIMKRFFFNIFTRQCEFIYGGCE 60
                                                                                                                                                                                                                                                                                         Production of tissue factor pathway inhibitor in yeast cells - with isolation from the insoluble cell fraction, used to treat or prevent
                                         tissue factor, Factor-Xa; binding protein; tissue factor inhibitor;
lipoprotein associated coagulation inhibitor;
extrinsic pathway inhibitor; sepsis; septic shock;
                                                                                                                                                                                                                                                                                                                                                         A mutein (AAR92012) of tissue factor pathway inhibitor (TFPI) is prepd. by site-directed mutagenesis of an encoding sequence. In the mutein, the lysine residue in the PI reactive site of the first Kunitz-type domain of TFPI is replaced by arginine. This domain is required for the inhibition of Factor-VIIa/Lissue factor (TF) complex. The mutein may be expressed in Saccharomyces cerevisiae transformants, esp. as a ubiquitin fusion protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Angiotensin converting enzyme (ACEV) splice variant protein #71.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     99.4%; Score 900; DB 17; Length 276; 99.4%; Pred. No. 1.2e-82;
                                  Tissue factor pathway inhibitor; TFPI; TFPI-2; Factor-VIIa;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         121 QCERFKYGGCLGNMNNFETLEECKNICEDGPNGFQVDNYGT 161
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             121 QCERFKYGGCLGNMNNFETLEECKNICEDGPNGFQVDNYGT 161
                                                                                                                                                                                                                                                                                                                                                                                                                                          and as a Factor-VIIa/TF/Xa binding protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Ą.
                                                                                                                                                                                                                                                                                                                                       Disclosure; Page 9; 36pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAU02971 standard; Protein; 225
                                                                                                                                                                       95WO-US09377
                                                                                                                                                                                              94US-0286530
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
                                                                               Saccharomyces cerevisiae.
                                                                                                                                                                                                                                                                                                              sepsis or septic shock
                                                                                                                                                                                                                                           Creasey AA, Innis MA;
                                                                                                                                                                                                                      (CHIR ) CHIRON CORP.
                                                                                                                                                                                                                                                                 WPI; 1996-129393/13.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  276 AA;
             TFPI mutein K36R
                                                                                                                                                                                              05-AUG-1994;
                                                                                                                          WO9604377-A1
                                                                                                                                                                       25-JUL-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           12-SEP-2001
                                                                                                                                                 15-FEB-1996,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Matches 160;
                                                                                                      Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAU02971;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAU0297
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Qγ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   qq
 ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         qq
```

```
The sequence represents an angiotensin converting enzyme splice variant (ACEV) polypeptide. The polypeptides of the invention include variants of granulocyte colony stimulating factor receptor, glucagon, interleukin 6, platelet-derived endothelial cell growth factor, cyclin-dependent kinase inhibitor IC, cellular tumour antigen PS3, and vasoative intestinal polypeptides and their associated nucleic acids are useful for identification of variant sequences and detection of candidate compounds capable of binding the molecules. The sequences of the invention can be used in the treatment and diagnosts of various consistince including cardiovascular diseases such as arteriosclerosis, myocardial infarction and coronary arterial thrombosis, renal diseases such as diabetic nephropathy, muscular diseases such as hypertropphy, immune complex nephritis, multiple sclerosis, cancer, sarcoidosis, nonarcoidottic pulmonary granulomatous diseases such as asbestosis and vascular pathologies involving an endothelial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Novel alternative splicing variants e.g. variant of anglotensin converting enzyme (ACEV), useful in identifying candidate compounds capable of binding to the variant and to detect anti-variant antibodies
vasoactive intestinal polypeptide receptor 2; arteriosclerosis; cancer; myocardial infarction; coronary arterial thrombosis; renal disease; diabetic nephropathy; muscular disease; immune disorder; sarcoidosis; multiple sclerosis; immune complex nephritis; deep vein thrombosis; nonarcoidotic pulmonary granulomatous disease; endothelial abnormality;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           61 GNONRFESLEECKKMCTRDNANRIIKTTLQQEKPDFCFLEEDPGICRGYITRYFYNQQTK 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      99 GNONRFESLEECKKMCTRDNANRIIKTTLQOEKPDFCFLEEDPGICRGYITRYFYNNOTK 148
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           88
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 DSEEDEEHTIITDIELPPLKLMHSFCAFKADDGPCRAIMKRFFFNIFTRQCEEFIYGGCE 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     29 DSEEDEEHTIITDTELPPLKLMHSFCAFKADDGPCKAIMKRFFFNIFTRQCEEFIYGGCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ;
;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 225;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Bernstein J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  149 QCERFKYGGCLGNMNNFETLEECKNICEDGPNGFQVDNYGT 189
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            121 QCERFKYGGCLGNMNNFETLEECKNICEDGPNGFQVDNYGT 161
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 897; DB 22;
Pred. No. 1.9e-82;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Levine Z, David A, Azar I, Khosravi R,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     abnormality such as deep vein thrombosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAW30311 standard; protein; 276 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 4; Fig 71; 519pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1;
                                                                                                                                                                                                           vascular disorder; asbestosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          99.18;
98.88;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            99IL-0132978.
99IL-0133455.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    17-NOV-2000; 2000WO-IL00766.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Matches 159; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (COMP-) COMPUGEN LID.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 2001-336004/35.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  225 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              N-PSDB; AAS06071
```

9

```
This sequence represents the human tissue factor pathway inhibitor (TPPI) protein. TPPI is also known as Lipoprotein-associated coagulation inhibitor (LACI), extrinsic pathway inhibitor (EPI) and Tissue factor inhibitor (TPI). The DNA encoding this sequence was altered to contain the optimum codons for expression in E. coli, to allow for expression of this protein in the bacteria. TPPI is used in the aqueous formulation of the invention. The aqueous formulation also includes a charged polymer (CP), preferably a sulphated polysaccharide (such as heparin or dextran sulphate) or a polyphosphate, preferably immobilised on a solid support. The CP is added to aid the correct refolding of TPPI. TPPI can also be modified or refolded using the methods of the invention. One method is for nedicting the solubility of a protein, by adding an aqueous solution of a CP to reduce inter- and intra-molecular interactions between the charged domains of the protein (e.g. TFPI), and comprises adding CP to a solution of the protein (e.g. TFPI), and comprises adding CP to a solution of the protein prior to allowing the protein to refold. The methods are particularly useful for solubilising, formulating, purifying and refolding proteins (especially TFPI) which have been engineered by genetic recombination and produced in bacterial, yeast or other cells in a form that has a non-native tertiary structure. TFPI is a coagulation inhibitor which has clot-inhibiting properties.
                                                                                   Tissue factor pathway inhibitor; TFPI; human; tissue factor inhibitor; ilpoprotein-associated coagulation inhibitor; coagulation inhibitor; TFI; LACI; extrinsic pathway inhibitor; protein refolding; clot-inhibitor; protein solubility modification; EPI.
                                                                                                                                                                                                                                           /note= "phosphorylated to varying degrees, but does not
  affect TFPI function"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         charged polymer, e.g. dextran sulphate, to facilitate solubilisation, formulation purification and refolding of protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Aq. formulation of tissue factor pathway inhibitor - contains
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gustafson ME;
Johnson K, Madani H;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Dorin GJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Chen B, Dorin GJ, ra MS, Johnson GV,
                                                                                                                                                                                                              Location/Qualifiers
                                                   Recombinant non-glycosylated TFPI.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Disclosure; Fig 4; 86pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Hora MS, Journal Hora MS, Tsang M;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             96WO-US09980
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              95US-0477677
95US-0473668
                  (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 t RF, hora
er. Rana RK,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 1997-087056/08.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Bild GS,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (CHIR ) CHIRON (SEAR ) SEARLE
                                                                                                                                                                                                                                                                                Disulfide-bond
                                                                                                                                                                                                                                                                                                                Disulfide-bond
Disulfide-bond
                                                                                                                                                                                                                                                                                                                                                                                                                        Disulfide-bond
                                                                                                                                                                                                                                                                                                  Disulfide-bond
                                                                                                                                                                                                                                                                                                                                                   Disulfide-bond
                                                                                                                                                                                                                                                                                                                                                                  Disulfide-bond
                                                                                                                                                                                                                                                                                                                                                                                      Disulfide-bond
                                                                                                                                                                                                                                                                                                                                                                                                    Disulfide-bond
                                                                                                                                                                                                                           Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                        WO9640784-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Pattison GL,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             07-JUN-1996;
                                                                                                                                                                           Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              07-JUN-1995;
07-JUN-1995;
                  30-JAN-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          19-DEC-1996.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Hallenbeck
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    BH,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Arve
```

276 AA;

Seguence

1

```
Human tissue factor pathway inhibitor; TFPI; TFPI-2; cell proliferation; angiogenesis-related disease; cancer; arthritis; macular degeneration;
                                                                       Gaps
                                              1 DSEEDEEHTIITDTELPPLKLMHSFCAFKADDGPCRAIMKRFFFNIFTRQCEEFIYGGCE
                                                                                                                                                                                                                                                                                                                                        "Kunitz-1 type protease inhibitor domain"
                                                                                                                                                                                                                                                                                                                                                                                      note= "Kunitz-2 type protease inhibitor domain"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       "Kunitz-3 type protease inhibitor domain"
                  ;
Length 276;
                  Indels
                                                                                                                                                                                                                                                                                                                         "Potential phosphorylation site"
                                                                                                            121 QCERFKYGGCLGNMNNFETLEECKNICEDGPNGFQVDNYGT 161
                                                                                                                     Score 897; DB 18;
Pred. No. 2.4e-82;
                                                                                                                                                                                                                                Human tissue factor pathway inhibitor (TFPI).
         Pred. No. 2.4e
1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                    /note= "N-glycosylated"
                                                                                                                                                                                                                                                                                                                                                                                                                         /note= "N-glycosylated"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /note= "N-glycosylated"
                                                                                                                                                                                                                                                                                                       Location/Qualifiers
                                                                                                                                                                         AAW61535 standard; protein; 276 AA
99.1%;
98.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Papathanassiu AE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          97US-0796850
                                                                                                                                                                                                              (first entry)
                                                                                                                                                                                                                                                                                                                                                                                            97..147
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                189..239
                  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                   122..143
                                                                                                                                                                                                                                                                                                                                                                                                                                                               239
                                                                                                                                                                                                                                                                                                                                                                              ..147
                                                                                                                                                                                                                                                                                                                         /note=
                                                                                                                                                                                                                                                                                                                                           'note=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note=
                                                                                                                                                                                                                                                                    diabetic retinopathy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (ENTR-) ENTREMED INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                            167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 1998-446947/38
         Similarity
                                                                                                                                                                                                                                                                                                                                                  Disulfide-bond
                                                                                                                                                                                                                                                                                                                                                                    Disulfide-bond
                                                                                                                                                                                                                                                                                                                                                                                               Disulfide-bond
Disulfide-bond
                                                                                                                                                                                                                                                                                                                                                                                                                                    Disulfide-bond
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Disulfide-bond
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Disulfide-bond
Disulfide-bond
                                                                                                                                                                                                                                                                                                                                                            Disulfide-bond
                                                                                                                                                                                                                                                                                                               Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                 Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                             Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Modified-site
                                                                                                                                                                                                                                                                                      Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WO9834634-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        06-FEB-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           06-FEB-1997;
                                                                                                                                                                                                              06-NOV-1998
         Best Local Sim
Matches 159;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       13-AUG-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Green SJ,
                                                                                                                                                                                             AAW61535;
 Query Match
                                                                                                                                                                                                                                                                                                                                                                                Domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Domain
                                                                                                                                                                                                                                                                                                                                  Domain
                                                                                                                                                         RESULT 6
                                                                                                                                                                 AAW61535
                                                                                                                                                                                    qq
                                                                         ŏ
                                                                                         g
                                                                                                            δ
                                                                                                                            g
```

us-09-741-106-19.rag

```
ö
                                                                                                 The present sequence represents the human tissue factor pathway inhibitor (TFPI). The invention provides compositions using TFPI and its homologs, e.g.TFPI-2 (AAM61586), for inhibiting cell proliferation. The compositions are claimed to be useful for inhibiting an angiogenesis-related disease, such as cancer, arthritis, macular
                                                                                                                                                                                                                                                                                                                                               61 GNONRFESLEECKKMCTRDNANRIIKTTLQQEKPDFCFLEEDPGICRGYITRYFYNQQTK 120
                                                                                                                                                                                                                                                                                                                                                               61 GNONRFESLEECKKMCTRDNANRIKTTLQQEKPDFCFLEEDPGICRGYITRYFYNNQTK 120
                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                        1 DSEEDEEHTIITDTELPPLKLMHSFCAFKADDGPCKAIMKRFFFNIFTRQCEEFIYGGCE 60
                                                                                                                                                                                                                                                                                         1 DSEEDEEHTIITDTELPPLKLMHSFCAFKADDGPCRAIMKRFFFNIFTRQCEEFIYGGCE 60
Composition comprising tissue factor pathway inhibitor for inhibiting cell proliferation - for treating anglogenesis related diseases e.g. cancer, arthritis, macular degeneration and diabetic retinopathy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Lipoprotein-associated coagulation inhibitor; LACI; kallikrein; inhibitor; KIP; Kunitz domain; hereditary angioedema.
                                                                                                                                                                                                                                                             ;
0
                                                                                                                                                                                                                                99.1%; Score 897; DB 19; Length 276; 98.8%; Pred. No. 2.4e-82;
                                                                                                                                                                                                                                                             Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Lipoprotein-associated coagulation inhibitor (LACI).
                                                                                                                                                                                                                                                                                                                                                                                                        QCERFKYGGCLGNMNNFETLEECKNICEDGPNGFQVDNYGT 161
                                                                                                                                                                                                                                                                                                                                                                                                                       121 QCEREKYGGCLGNMNNFETLEECKNICEDGPNGFQVDNYGT 161
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 "Kunitz domain LACI-K2"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "Kunitz domain LACI-K1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /note= "Kunitz domain LACI-K3"
                                                                                                                                                                                                                                                             1; Mismatches
                                                                                                                                                                          degeneration or diabetic retinopathy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1..28
/label= sig_peptide
                                                                         Claim 6; Pages 23-24; 37pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAR81884 standard; protein; 304 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  95WO-US00299
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           94US-0179964
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             94US-0208264
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   121..178
/note= "Ki
213..270
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (PROT-) PROTEIN ENG CORP.
                                                                                                                                                                                                                                               Best_Local Similarity 98.8
Matches 159; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Markland W;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /note=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 1995-292934/38
                                                                                                                                                                                                       276 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  11-JAN-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           11-JAN-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WO9521601-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             10-MAR-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                18-MAR-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      17-AUG-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Ladner RC,
                                                                                                                                                                                                       Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAR81884
                                                                                                                                                                                                                                   Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Domain
                                                                                                                                                                                                                                                                                                                                                                                                         121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     g
    ŏ
                                                                                                                                                                                                                                                                                                                     요
                                                                                                                                                                                                                                                                                                                                                  ð
                                                                                                                                                                                                                                                                                                                                                                                                         δ
                                                                                                                                                                                                                                                                                                                                                                                                                                    염
```

```
AAR81884 is the human lipoprotein-associated coagulation inhibitor LACI. The Kunitz domain, LACI-KI, of LACI is a kallikrein inhibiting protein (KIP) upon which the claimed KIPs of the invention are based. The KIPs can be used for treating or preventing disorders attributable to excessive kallikrein activity, e.g. hereditary angloedema. The KIPs can also be used for assaying, purifying and in vivo imaging of kallikrein.
                                                                                                                                                                                                                                                                                                                                                                             GNONRFESLEECKKMCTRDNANRIIKTTLQQEKPDFCFLEEDPGICRGYITRYFYNQQTK 120
                                                                                                                                                                                                                                                                                                                      29 DSEEDEEHTIITDTELPPLKLMHSFCAFKADDGPCKAIMKRFFFNIFTRQCEEFIYGGCE 88
Kallikrein inhibiting proteins comprising a Kunitz domain homologous to bovine pancreatic trypsin inhibitor - useful for preventing or treating disorders attributable to excessive kallikrein activity,
                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                     1 DSEEDEEHTIITDTELPPLKLMHSFCAFKADDGPCRAIMKRFFFNIFTRQCEEFIYGGCE 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Yeast aspartic protease 3; YAP3; signal peptide; protein secretion; tissue factor pathway inhibitor; TFPI.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DNA construct encoding the yeast aspartic protease 3 signal peptide - provides improved secretion of proteins in transformed yeast cells, such as aprotinin and insulin
                                                                                                                                                                                                                                                                          .;
0
                                                                                                                                                                                                                                              Length 304;
                                                                                                                                                                                                                                                                         Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                      149 QCERFKYGGCLGNMNNFETLEECKNICEDGPNGFQVDNYGT 189
                                                                                                                                                                                                                                                                                                                                                                                                                       QCERFKYGGCLGNMNNFETLEECKNICEDGPNGFQVDNYGT 161
                                                                                                                                                                                                                                              Score 897; DB 16;
Pred. No. 2.7e-82;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     | 1.28
|/label= Sig_peptide
|/^orte= "TFPI signal peptide"
                                                                                                                                                                                                                                                                          1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Location/Qualifiers
                                                                         Disclosure; Page 24; 46pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAR67994 standard; Protein; 304 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Tissue factor pathway inhibitor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Christiansen L, Petersen JG;
                                              eg, in hereditary angioedema.
                                                                                                                                                                                                                                               99.1%;
98.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             94WO-DK00281
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      93DK-0000828
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                13-AUG-1995 (first entry)
                                                                                                                                                                                                                                                                            Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (NOVO ) NOVO-NORDISK AS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 1995-066903/09.
N-PSDB; AAQ81396.
                                                                                                                                                                                                                                                             Similarity
                                                                                                                                                                                                                   304 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           08-JUL-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        08-JUL-1993;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WO9502059-A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               19-JAN-1995
                                                                                                                                                                                                                                                                          Matches 159;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAR67994;
                                                                                                                                                                                                                      Sequence
                                                                                                                                                                                                                                               Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Peptide
                                                                                                                                                                                                                                                                Local
                                                                                                                                                                                                                                                                                                                                                                                            89
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             æ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAR67994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   QQ
                                                                                                                                                                                                                                                                                                                                                                 δλ
                                                                                                                                                                                                                                                                                                                                                                                          g
                                                                                                                                                                                                                                                                                                                                                                                                                        ŏ
                                                                                                                                                                                                                                                                                                                                                                                                                                                  g
                                                                                                                                                                                                                                                                                                        δ
```

ö

ó

```
;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAZ32159 to AAZ32194 represent reference alleles for specifically claimed nucleic acid sequences from the present invention which comprise bolymorphic sites as given in a table in the specification, selected from 92 single nucleotide polymorphisms in which the nucleotide at the polymorphic site is different from a nucleotide at the same site in a reference allele. The nucleic acids, and primers and probes, are used to identify polymorphisms, which may predispose an individual to disease, sepecially a vascular disease. They can also be used in phenotype correlations, forensics, paternity testing, medicine or genetic analysis. AAY49550 to AAY49573 represent the proteins which correspond
                                                                                                                                                                                                                                                                                                              61 GNQNRFESLEECKKMCTRDNANRIIKTTLQQEKPDFCFLEEDPGICRGYITRYFYNQQTK 120
                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human; coding sequence polymorphism; vascular pathology gene; polymorphic site; phenotype correlation; forensic; paternity testing; medicine; genetic analysis; vascular disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Determination of polymorphisms in genes, especially those identifying predisposition to vascular disease
                                                                                                                                                                                                                                                               29 DSEEDEEHTIITDTELPPLKLMHSFCAFKADDGPCKAIMKRFFFNIFTRQCEEFIYGGCE 88
                                                                                                                                                                                                                                             1 DSEEDEEHTIITDTELPPLKLMHSFCAFKADDGPCRAIMKRFFFNIFTRQCEEFIYGGCE 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human lipoprotein associated coagulation inhibitor protein sequence.
                                A SalI fragment encoding human tissue factor pathway inhibitor (TFPI) is given in AA081396. It was used to contruct expression vectors allowing production of FFPI in Saccharomyces cerevisae as fusions to the yeast aspartic protease 3 (YAP3) signal peptide, facilitating secretion of the recombinant TFPI.
                                                                                                                                                                                                                ö
                                                                                                                                                                               Length 304;
                                                                                                                                                                                                                1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Rozen SG;
                                                                                                                                                                                                                                                                                                                                                                                                 149 QCERFKYGGCLGNMNNFETLEECKNICEDGPNGFQVDNYGT 189
                                                                                                                                                                                                                                                                                                                                                                               121 OCERFKYGGCLGNMNNFETLEECKNICEDGPNGFQVDNYGT 161
                                                                                                                                                                            Score 897; DB 16;
Pred. No. 2.7e-82;
1; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Cargill M, Ireland JS,
Disclosure; Page 27-28; 56pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (WHED ) WHITEHEAD INST BIOMEDICAL RES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAY49557 standard; Protein; 304 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Disclosure; Fig 10; 134pp; English.
                                                                                                                                                                          99.1%;
98.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      99WO-US06473.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      98US-0054272
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (first entry)
                                                                                                                                                                                                          Matches 159; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Lander ES, Daley GQ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 1999-620066/53.
                                                                                                                                                                                              Best Local Similarity
                                                                                                                                           304 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            N-PSDB; AAZ32166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            13-JAN-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WO9950454-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    26-MAR-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-APR-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   07-0CT-1999
                                                                                                                                           Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAY49557;
                                                                                                                                                                            Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT
                                                                                                                                                                                                                                                                            셤
 g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         à
                                                                                                                                                                                                                                                                                                              ò
                                                                                                                                                                                                                                                                                                                                                                                 ò
                                                                                                                                                                                                                                                                                                                                                                                                                g
```

```
61 GNONRFESLEECKKMCTRDNANRIIKTTLQQEKPDFCFLEEDPGICRGYITRYFYNQQTK 120
                                                                                                                                                                      Gaps
                                                                                                      1 DSEEDEEHTIITDTELPPLKLMHSFCAFKADDGPCRAIMKRFFFNIFTRQCEEFIYGGCE 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Production of tissue factor pathway inhibitor in yeast cells - with isolation from the insoluble cell fraction, used to treat or prevent sepsis or septic shock
                                                                                                                                                                                                                                                                                                                                                                                                                    tissue factor; Factor-Xa; binding protein; tissue factor inhibitor;
lipoprotein associated coagulation inhibitor;
extrinsic pathway inhibitor; sepsis; septic shock;
                                                                                                                   A ubiquitin/tissue factor pathway inhibitor (TFPI) fusion protein (AAR92011) is produced within Saccharomyces cerevisiae host cells
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /note= "amino acids 77-352 comprise mature TFPI"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /note= "amino acids 1-73 comprise the ubiquitin
                                                                                .;
0
                                                      Length 304;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       "amino acids 74-76 comprise a linker
                                                                                                                                                                                                                                                                                                                                                                                                      Tissue factor pathway inhibitor; TFPI; TFPI-2; Factor-VIIa;
                                                                              Indels
                                                                                                                                                                                                                        149 QCERPKYGGCLGNMNNFETLEECKNICEDGPNGFQVDNYGT 189
                                                                                                                                                                                                         121 QCERFKYGGCLGNMNNFETLEECKNICEDGPNGFQVDNYGT 161
                                                   99.1%; Score 897; DB 20; 98.8%; Pred. No. 2.7e-82;
                                                                 Pred. No. 2.76
1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               fusion partner"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Disclosure; Page 20-22; 36pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Location/Qualifiers
                                                                                                                                                                                                                                                                                                  AAR92011 standard; Protein; 352 AA.
 to some of the reference alleles.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    sedneuce,
                                                                                                                                                                                                                                                                                                                                                                            Ubiquitin-TFPI fusion protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        95WO-US09377
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 94US-0286530.
                                                                                                                                                                                                                                                                                                                                                   08-MAY-1996 (first entry)
                                                                             Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Saccharomyces cerevisiae.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /note=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Chimeric Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Creasey AA, Innis MA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (CHIR ) CHIRON CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 1996-129393/13.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Chimeric synthetic;
                                                                Similarity
                         304 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           N-PSDB; AAT16056
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WO9604377-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       25-JUL-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 05-AUG-1994;
                                                                Best Local Sim
Matches 159;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               15-FEB-1996
                           Seguence
                                                                                                                                                                                                                                                                                                                          AAR92011;
                                                   Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Protein
                                                                                                                                                                                                                                                                         RESULT 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Key
                                                                                                                                                                                                                                                                                    AAR92011
SXC
                                                                                                                                                                                                                                                                                                                          g
                                                                                                                                                        δλ
                                                                                                                                                                               q
                                                                                                                                                                                                          δŏ
                                                                                                                                                                                                                                Dp
```

Gaps

.; o

Indels

ij

1; Mismatches

Conservative

```
Matches 158;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Key
Region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Region
                                                                                         61
                                                                                                                                                 121
                                                                                                                                                                                                                           RESULT 12
                                                                                                                                                                                                                                          AAP92002
                                                        g
                                                                                                                     g
                                                                                                                                                 δ
                                                                                         ŏ
                                                                                                                                                                  ö
                                                                                                                                                                                                                77 DSEEDEEHTIITDTELPPLKLMHSFCAFKADDGPCKAIMKRFFFNIFTRQCEEFIYGGCE 136
                                                                                                                                                                                                                                                        61 GNQNRFESLEECKKMCTRDNANRIIKTTLQQEKPDFCFLEEDPGICRGYITRYFYNQQTK 120
                                                                                                                                                                                                                                                                          The sequence given is a peptide fragment of lipoprotein-associated coaglutination inhibitor (IACI) having the sequence of residues 1 to 160 of the 276 residue mature LACI protein. This peptide fragment corresponds to Kunitz domains of LACI and can be used for
                                                                                                                                                                  Gaps
                                                                                                                                                                                              1 DSEEDEEHTIITDTELPPLKLMHSFCAFKADDGPCRAIMKRFFFNIFTRQCEEFIYGGCE 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Peptide fragments of lipoprotein-associated coagulation inhibitor - used for inhibiting Factor Xa prodn. or inhibiting Factor VIIA tissue factor complex formation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  inhibiting Factor VIIa/tissue factor enzymatic complex formation Factor VIIa is the activated form of factor VII.
following transformation with vector plasmid pLACI 4.1, which carries a ubiquitin/TFPI gene fusion (AAT16056). The fusion protein is cleaved within the yeast cell, so that mature TFPI having an authentic N-terminal sequence (see AAR2013) is obtd. Max. prodn. of TFPI from yeast transformants reached I mg/ml. TFPI is used to treat or prevent sepsis and septic shock.
                                                                                                                                                                  ő
                                                                                                                                   Ouery Match 99.1%; Score 897; DB 17; Length 352; Best Local Similarity 98.8%; Pred. No. 3.3e-82; Matches 159; Conservative 1; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Lipoprotein-associated coaglutination inhibitor; kuintz.
                                                                                                                                                                                                                                                                                                                                  197 QCERFKYGGCLGNMNNFETLEECKNICEDGPNGFQVDNYGT 237
                                                                                                                                                                                                                                                                                                                  121 QCERFKYGGCLGNMNNFETLEECKNICEDGPNGFQVDNYGT 161
                                                                                                                                                                                                                                                                                                                                                                                                                         AAR23800 standard; Protein; 160 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Disclosure; Fig 1; 9pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            87US-0077366.
87US-0123753.
89US-0301779.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   89US-0301779
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (UNIW ) UNIV WASHINGTON.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LACI fragment 1 - 160.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Broze GJ, Girard TJ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 1992-159405/19.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 160 AA;
                                                                                                        352 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 26-JAN-1989;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               23-JUL-1987;
23-NOV-1987;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             26-JAN-1989;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     03-NOV-1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US5106833-A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      21-APR-1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAR23800
                                                                                                          Sequence
                                                                                                                                                                                                                                                                                                                                                                                            RESULT 11
                                                                                                                                                                                                                                                                                                                                                                                                           AAR23800
                                                                                                                                                                                                                                                                                                                                                                                                                                                      88888888888
                                                                                                                                                                                                ď
                                                                                                                                                                                                                            QQ
                                                                                                                                                                                                                                                          ŏ
                                                                                                                                                                                                                                                                                    g
                                                                                                                                                                                                                                                                                                                    ŏ
                                                                                                                                                                                                                                                                                                                                             g
```

Score 892; DB 13; Length 160; Pred. No. 4.1e-82;

98.68; 98.88;

Query Match Best Local Similarity

```
Human tissue factor inhibitor; TFI; human placenta lambda-P9 clone; basic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Amino acid sequence of tissue factor inhibitor (TFI) cDNA isolate from lambda-P9 clone of human placenta cDNA library. Domains discerned
                                                               GNONRFESLEECKKMCTRDNANRIIKTTLQQEKPDFCFLEEDPGICRGYITRYFYNQQTK 120
1 DSEEDEEHT LITDTELPPLK LAHSFCAFKA DGPCRAIMKRFFFNIFTRQCEEFIYGGCE 60
              1 DSEEDEEHTIITDTELPPLKLMHSFCAFKADDGPCKAIMKRFFFNIFTRQCEEFIYGGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /note= "Potential N-linked glycosylation site"
31..53
                                                                                                                                                                                                                                                                                                                                                                                                                                                             /note= "Potential N-linked glycosylation site"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note= "Potential N-linked glycosylation site"
                                                                                                                                                                                                                                                                                                                                                                                                                      'note= "Possible site for signal peptidase"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DNA encoding human tissue factor inhibitor - used in study of coagulation cascade for agents which inhibit factor Xa and Factor VIIA-TF
                                                                                                    QCERFKYGGCLGNMNNFETLEECKNICEDGPNGFQVDNYG 160
                                                                                                                121 QCERFKYGGCLGNMNNFFTLEECKNICEDGPNGFQVDNYG 160
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /note= "See comments below"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /note= "See comments below"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note= "See comments below
                                                                                                                                                                                                                                                                                                                                                                       1..28
/label= Signal_region
/note= "A-T rich"
                                                                                                                                                                                                                                                                     Human tissue factor inhibitor (TFI).
                                                                                                                                                                                                                                                                                                          protease inhibitor gene superfamily
                                                                                                                                                                                                                                                                                                                                                            Location/Qualifiers
                                                                                                                                                                                            ¥.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 3; Figure 3; 14pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Wun TC;
                                                                                                                                                                                          AAP92002 standard; protein; 304
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    88EP-0870127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             87US-0123753
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (MONS ) MONSANTO CO (UNIW).
                                                                                                                                                                                                                                             09-FEB-1990 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         .197
                                                                                                                                                                                                                                                                                                                                                                                                                                                  145..147
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  . 88.
                                                                                                                                                                                                                                                                                                                                                                                                                                     ..304
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             153..16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Kretzmer KK,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 1989-159483/22.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   N-PSDB; AAN90108.
                                                                                                                                                                                                                                                                                                                                                                                                              Cleavage-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     22-JUL-1988;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             23-NOV-1987;
                                                                                                                                                                                                                                                                                                                                    Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            31-MAY-1989
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EP318451-A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Broze GJ,
                                                                                                                                                                                                                    AAP92002;
```

```
ò
include: highly negatively charged N-terminal; highly positively charged carboxy-terminal; intervening portion consisting of 3 homologous domains with sequences typical of Kunitz-type enzyme inhibitors. Based on homology study, it appears to be a member of the basic protease inhibitor gene superfamily. Sequences in misc. regions in feature table above have been independently confirmed by amino acid sequence analysis.
                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                   61 GNQNRFESLEECKKMCTRDNANRIIKTTLQQEKPDFCFLEEDPGICRGYITRYFYNQQTK 120
                                                                                                                                                                                                                        kunitz domains of native EPI and have one or more amino acids deleted in the region Glu148 to the C-terminal Met276, especially in the region from Arg246 to Ly8275. This analogue is an example of such a peptide; it corresponds to amino acids 1 to 255 of native EPI with an additional N-terminal Ser residue. The analogue can be used in a therapeutic composition to treat patients having coagulation disorders or cancer. The analogue has a longer half-life than
                                                                                                                                                                                                     1 DSEEDEEHTIITDTELPPLKLMHSFCAFKADDGPCRAIMKRFFFNIFTRQCEEFIYGGCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Extrinsic pathway inhibitor protein; tissue plasminogen activator; kunitz domain; coagulation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Preferred EPI analogues of the invention comprise the first two
                                                                                                                                                                            ö
                                                                                                                                            Score 891; DB 10; Length 304;
Pred. No. 1.1e-81;
1; Mismatches 2; Indels C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Extrinsic pathway inhibitor protein analogue - useful as anticoagulant and anti-cancer agent due to low or no
                                                                                                                                                                                                                                                                                                                               121 QCERFKYGGCLGNMNNFETLEECKNICEDGPNGFQVDNYGT 161
                                                                                                                                                                                                                                                                                                                                                 149 QCERFKYGGCLGNMNNFETLEECKNICEDGPNGFQVDNYGT 189
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 See also AAQ10992-4 and AAR11170-R11172.
                                                                                                                                                                                                                                                                                                                                                                                                                                         AAR11169 standard; Protein; 256 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 5; Page 20; 39pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Ser(Aspl-Thr255) - EPI analogue.
                                                                                                                                            98.5%;
98.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          90WO-DK00212.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        89DK-0004080
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (first entry)
                                                                                                                                                                         Matches 158; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (NOVO ) NOVO NORDISK A/S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Nordfang O;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              heparin-binding capacity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 1991-087248/12.
                                                                                                                                          Query Match
Best Local Similarity
                                                                                                             304 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                256 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Rasmussen J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         17-AUG-1990;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        18-AUG-1989;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       21-MAY-1991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WO9102753-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          07-MAR-1991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Synthetic
                                                                                                              Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAR11169;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence
                                                                                                                                                                                                                                    53
                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 13
                                                                                                                                                                                                                                                                                                                                                                                                                          AAR11169
   8888888
                                                                                                                                                                                                                                    g
                                                                                                                                                                                                                                                                                              g
                                                                                                                                                                                                                                                                                                                                                                                                                                          ð
                                                                                                                                                                                                                                                                   ò
                                                                                                                                                                                                                                                                                                                             ò
                                                                                                                                                                                                                                                                                                                                                            임
```

```
61 GNONRFESLEECKKMCTRDNANRIIKTTLQQEKPDFCFLEEDPGICRGYITRYFYNQQTK 120
                                                                                                                                               62 GNONRFESLEBCKKMCTRDNANRIIKTTLQQEKPDFCFLEEDPGICRGYITRYFYNNOTK 121
                                    Gaps
                                                               1 DSEEDEEHTIITDTELPPLKLMHSFCAFKADDGPCRAIMKRFFFNIFTRQCEEFIYGGCE 60
                                                                                                61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 DSEEDEEHTIITDTELPPLKLMHSFCAFKADDGPCRAIMKRFFFNIFTRQCEEFIYGGCE 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2 DSBEDEEHTIITDTBLPPLKLMHSFCAFKADDGPCKAIMKRFFFNIFYRQCEEFIYGGCE 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  kunitz domains of native EPI and have one or more amino acids deleted in the region Glu148 to the C-terminal Mer276, especially in the region from Arg246 to L6375. This analogue is an example of such a peptide; it has amino acids 246 to 261 of native EPI deleted with an optional N-terminal Ser residue. The analogue can be used in a therapeutic composition to treat patients having coagulation disorders or cancer. The analogue has a longer half-life than
                                                                                                                                                                                                                                                                                                                                                                                                                                    pathway inhibitor protein; tissue plasminogen activator;
                                                                                2 DSEEDEEHTIITDTELPPLKLMHSFCAFKADDGPCKAIMKRFFFNIFYRQCEEFIYGGCE
                                   0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Preferred EPI analogues of the invention comprise the first two
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 .
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 261;
   Length 256;
                                   Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Extrinsic pathway inhibitor protein analogue - useful as anticoagulant and anti-cancer agent due to low or no heparin-binding capacity
                                                                                                                                                                                            121 QCERFKYGGCLGNMNNFETLEECKNICEDGPNGFOVDNYGT 161
                                                                                                                                                                                                           122 QCERFKYGGCLGNMNNFETLEECKNICEDGPNGFQVDNYGT 162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          See also AAQ10992-4 and AAR11169-R11170, AAR11172.
Score 890; DB 12;
Pred. No. 1.1e-81;
1; Mismatches 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 890; DB 12;
Pred. No. 1.2e-81;
                                                                                                                                                                                                                                                                                                                                                                                                    Ser-(Asp1-Glu245)-(Glu262-Met276)-EPI analogue.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1; Mismatches
                                                                                                                                                                                                                                                                                                     AAR11171 standard; Protein; 261 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 5; Page 20; 39pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              98.3%;
98.1%;
 98.3%;
98.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                90WO-DK00212.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            89DK-0004080.
                                                                                                                                                                                                                                                                                                                                                                                                                                                   kunitz domain; coaqulation
                                                                                                                                                                                                                                                                                                                                                                      (first entry)
                                 Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Rasmussen J, Nordfang O;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (NOVO ) NOVO NORDISK A/S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Matches 158; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 1991-087248/12.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Similarity
                Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               261 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  full-length EP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            17-AUG-1990;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            18-AUG-1989;
                                                                                                                                                                                                                                                                                                                                                                      21-MAY-1991
                              Matches 158;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WO9102753-A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                07-MAR-1991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                    Extrinsic
                                                                                                                                                                                                                                                                                                                                      AAR11171;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sednence
   Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Local
                                                                                                                                                                                                                                                                       RESULT 14
                                                                                                                                                                                                                                                                                      AAR1117
                                                                                                                                                                                                                                                                                                                                     음
                                                               öλ
                                                                                                                             ò
                                                                                                                                                       D.
                                                                                                                                                                                          ŏ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          δλ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       q
```

; 0

.

```
ò
1 DSEEDBEHTIITDTELPPLKLMHSFCAFKADDGPCRAIMKRFFFNIFTRQCEEFIYGGCE 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2 DSEEDEEHTIITDTELPPLKLMHSFCAFKADDGPCKAIMKRFFFNIFYRQCEEFIYGGCE 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Preferred EPI analogues of the invention comprise the first two kunitz domains of native EPI and have one or more amino acids deleted in the region Glu148 to the C-terminal Met276, especially in the region from Arg246 to Lys275. This analogue is an example of such a peptide; it has amino acids 249 to 263 of native EPI deleted with an optional N-terminal Ser residue. The analogue can be used in a therapoutic composition to treat patients having coagulation disorders or cancer. The analogue has a longer half-life than
                                                                                                                                                                                                                                                             Extrinsic pathway inhibitor protein; tissue plasminogen activator;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        .;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 890; DB 12; Length 262;
Pred. No. 1.2e-81;
1; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   as
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Extrinsic pathway inhibitor protein analogue - useful anticoagulant and anti-cancer agent due to low or no heparin-binding capacity
                                                                    122 QCERFKYGGCLGNMNNFFTLEECKNICEDGPNGFQVDNYGT 162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            122 QCERFKYGGCLGNMNNFETLEECKNICEDGPNGFQVDNYGT 162
                                                    121 QCERFKYGGCLGNMNNFETLEECKNICEDGPNGFQVDNYGT 161
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              OCERFKYGGCLGNMNNFETLEECKNICEDGPNGFQVDNYGT 161
                                                                                                                                                                                                                                     Ser-(Asp1~Ser248)-(Val264-Met276)-EPI analogue.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       See also AAQ10992-4 and AAR11169-R11171.
                                                                                                                                                 AAR11172 standard; Protein; 262 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 5; Page 20; 39pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ij
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            98.3%;
98.1%;
                                                                                                                                                                                                                                                                                                                                                                                         90WO-DK00212
                                                                                                                                                                                                                                                                                                                                                                                                                   89DK-0004080
                                                                                                                                                                                                                                                                             kunitz domain; coaqulation
                                                                                                                                                                                                        21-MAY-1991 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Nordfang 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                              (NOVO ) NOVO NORDISK A/S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 1991-087248/12.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  262 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Rasmussen J,
                                                                                                                                                                                                                                                                                                                                                                                       17-AUG-1990;
                                                                                                                                                                                                                                                                                                                                                                                                                   18-AUG-1989;
                                                                                                                                                                                                                                                                                                                                  WO9102753-A.
                                                                                                                                                                                                                                                                                                                                                             07-MAR-1991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Best Local Sim
Matches 158;
                                                                                                                                                                                                                                                                                                        Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence
                                                                                                                                                                              AAR11172;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              121
                                                                                                                           RESULT 15
                         g
                                                      ŏ
                                                                             d
                                                                                                                                                                 OD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       δy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 q
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ò
```

```
Search completed: December 2, 2002, 10:02:25 Job time: 73.0896 secs
```

```
Appl
Appl
Appl
Appl
Appli
Appli
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Appli
Appli
Appli
Appli
Appli
Appli
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Appli
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Appli
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Appli
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Appl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Appl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 19, Appl
Sequence 19, Appl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Appli
                                                                           (without alignments)
179.212 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                     Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 18,
Sequence 18,
Sequence 1, A
                                                                 December 2, 2002, 10:02:30 ; Search time 26.4328 Seconds
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 19,
Sequence 19,
Sequence 19, A
Sequence 9, A
Sequence 9, A
Sequence 3, A
Sequence 9, A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 25,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 1,
                                                                                                                                 1 DSEEDEEHTIITDTELPPLK......ECKNICEDGPNGFQVDNYGT 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 9,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Description
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence Sequence 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence
                                                                                                                                                                                                                                                                                                                        /cgn2_6/ptodata/1/iaa/5A_COMB.pep:*
/cgn2_6/ptodata/1/iaa/5B_COMB.pep:*
/cgn2_6/ptodata/1/iaa/6A_COMB.pep:*
/cgn2_6/ptodata/1/iaa/6B_COMB.pep:*
/cgn2_6/ptodata/1/iaa/PcTUS_COMB.pep:*
/cgn2_6/ptodata/1/iaa/PcTUS_COMB.pep:*
            Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-08-437-841-19
US-08-286-521-19
US-08-43-682-19
US-08-43-682-19
US-08-437-841-9
US-08-436-519
US-08-86-521-9
US-08-86-521-9
US-08-86-521-9
US-08-86-175-9
US-08-86-175-9
US-08-943-682-9
PCT-USSS-09464-9
US-08-96-850-1
US-08-08-646-9
US-08-08-646-9
US-08-145-2
US-08-145-2
US-08-145-2
US-08-126-188-18
US-08-126-188-18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-08-676-124-1
US-08-208-264A-25
US-09-414-878-1
US-09-240-136-1
US-09-421-097-25
GenCore version 5.1.3
Copyright (c) 1993 - 2002 Compug
                                                                                                                                                                                                          Total number of hits satisfying chosen parameters:
                                                                                                                                                                                       262574 segs, 29422922 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                  SUMMARIES
                                                                                                                                                                                                                                                                   Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                            - protein search, using sw model
                                                                                                                                                                 Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                                                                                                Issued_Patents_AA:*
                                                                                                                                                                                                                                 Minimum DB seq length: 0 Maximum DB seq length: 2000000000
                                                                                                             US-09-741-106-19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               BLOSUM62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query
Match 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   . . . . . . . . . .
                                                                                                                                                        Scoring table:
                                                                                                            Title:
Perfect score:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  88977
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    8897
8897
8897
8897
8897
8897
8897
                                             OM protein
                                                                                                                                                                                                                                                                                                                Database :
                                                                                                                                                                                        Searched:
                                                                                                                                   Sequence:
                                                                  Run on:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Result
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Š
```

```
1, Appli
5, Appli
5466783
                                                            Appli
                                                                        , Appl
Appli
, Appl
                                                                                                           Appl
Appl
Appl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                  Sequence 5, A
Patent No. 546
Sequence 3, A
Sequence 12,
                                                                                                         Sequence
Sequence
Sequence
                                                                                                                                                                              Sequence
             Sequence
                                                                                   Sequence
                                                                                             Sequence
                                                                                                                                            Sequence
                                                                                                                                                       Sequence
                                                                                                                                                                    Sequence
                                                                                                                                                                                                       Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 161;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30B
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/437,841
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 100.0%; Score 905; DB 1; Best Local Similarity 100.0%; Pred. No. 1.1e-92; Matches 161; Conservative 0; Mismatches 0;
         US-09-054-782-2

US-07-828-920A-1

US-07-828-920A-5

546678-25

US-07-828-920A-3

US-08-321-658B-12

US-08-321-658B-12

US-08-331-658B-8

US-08-331-658B-8

US-08-384-489-14

US-08-384-489-14

US-08-384-385

US-08-463-155A-36

US-08-463-155A-36

US-08-206-310A-36

US-08-398-610A-36

US-08-398-628A-36

US-08-398-628A-36

US-08-398-628A-36

US-08-398-628A-36

US-08-398-628A-36

US-08-398-628A-36

US-08-398-628A-36

US-08-398-628A-36
                                                                                                                                                                                                                                       ALIGNMENTS
                                                                                                                                                                                                                                                                                              Sequence 19, Application US/08437841
Patent No. 5563123
GENERAL INFORMATION:
APPLICANT: Innis, Michael
APPLICANT: Creasey, Abla
TITLE OF INVENTION: Chimeric Proteins
NUMBER OF SEQUENCES:
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME: Savereide, Paul B.
REGISTRATION NUMBER: 36,914
REFERENCE_POCKET NUMBER: 0990.001
TELECOMMUNICATION INFORMATION:
TELECHONE: 510-601-2585
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/286,521
FILING DATE: 05-AUG-1994
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                Chiron Corporation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           161 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEFAX: 510-655-3542 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                          4560 Horton St
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STRANDEDNESS: single
MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                       Emeryville
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CLASSIFICATION:
USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                        94608
                                                                                                                                                                                                                                                                                                                                                                                                ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                   CA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TOPOLOGY:
                                                                                                                                                                                                                                                                          RESULT 1
US-08-437-841-19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-08-437-841-19
                                                                                                                                                                                                                                                                                                                                                                                                          STREET:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                             COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                  STATE:
 \frac{2}{2}
```

1 DSEEDEEHTIITDTELPPLKLMHSFCAFKADDGPCRAIMKRFFFNIFTRQCEEFIYGGCE 60

δŏ

Patent No. 5466783 Sequence 2, Appli Sequence 2, Appli

US-08-854-764-2 PCT-US95-09377-2 US-09-638-770A-1

Appl

Sequence 25,

Sequence

```
g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 δλ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        61 GNQNRFESLEECKKMCTRDNANRIIKTTLQQEKPDFCFLEEDPGICRGYITRYFYNQQTK 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                61 GNONRFESLEECKKMCTRDNANRIKTTLQQEKPDFCFLEEDPGICKGYITRYFYNQOTK 120
                                                                                                               61 GNONRFESLEECKKMCTRDNANRIIKTTLQQEKPDFCFLEEDPGICRGYITRYFYNQOFK 120
                                                                           61 GNONRFESLEECKKMCTRDNANRIIKTTLQQEKPDFCFLEEDPGICRGYITRYFYNQQTK 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 DSEEDEEHTIITDIELPPLKLMHSFCAFKADDGPCRAIMKRFFFNIFTRQCEEFIYGGCE 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 DSEEDEEHTIITDTELPPLKLMHSFCAFKADDGPCRAIMKRFFFNIFTRQCEFIYGGCE 60
1 DSEEDEEHTIITDTELPPLKLMHSFCAFKADDGPCRAIMKRFFFNIFTRQCEFFIYGGCE 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             100.0%; Score 905; DB 1; Length 161; 100.0%; Pred. No. 1.1e-92;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30B
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/286,521
FILING DATE: 05-AUG-1994
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Saveraide, Paul B.
RESIERNCE/DOCKET NUMBER: 36,914
REFERENCE/DOCKET NUMBER: 36,914
REF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            121 QCERFKYGGCLGNMNNFETLEECKNICEDGPNGFQVDNYGT 161
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    121 QCERFKYGGCLGNMNNFETLEECKNICEDGPNGFQVDNYGT 161
                                                                                                                                                                                                                                   121 QCERFKYGGCLGNMNNFETLEECKNICEDGPNGFQVDNYGT 161
                                                                                                                                                                                                                                                                       121 QCERFKYGGCLGNMNNFETLEECKNICEDGPNGFQVDNYGT 161
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Innis, Michael
APPLICANT: Creasey, Abla
TITLE OF INVENTION: Chimeric Proteins
NUMBER OF SEQUENCES: 37
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 19, Application US/08436175 Patent No. 5696088
                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-08-286-521-19; Sequence 19, Application US/08286521
patent No. 5589359; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Chiron Corporation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ADDRESSEE: Chilon -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Matches 161; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STREET: 4500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 3
US-08-436-175-19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-08-286-521-19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT 2
                                                                                                                                                   qq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            á
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   g
                                                                               ò
                                                                                                                                                                                                                                   δy
```

```
61 GNQNRFESLEECKKMCTRDNANRIIKTTLQQEKPDFCFLEEDPGICRGYITRYFYNQQTK 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       61 GNONRFESLEECKKMCTRDNANRIKTTLQQEKPDFCFLEEDPGICRGYITRYFYNQQTK 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 DSEEDEEHTIITDTELPPLKLMHSFCAFKADDGPCRAIMKRFFFNIFTRQCEFFIYGGCE 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 DSEEDEEHTIITDTELPPLKLMHSFCAFKADDGPCRAIMKRFFFNIFTRQCEEFIYGGCE 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      100.0%; Score 905; DB 1; Length 161; 100.0%; Pred. No. 1.1e-92; Live 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compartible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30B
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     121 QCERFKYGGCLGNMNNFETLEECKNICEDGPNGFQVDNYGT 161
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 19, Application US/08943682
Patent No. 6174721
GENERAL INFORMATION:
APPLICANT: Innis, Michael
APPLICANT: Creasey, Abla
TITLE OF INVENTION: Chimeric Proteins
NUMBER OF SEQUENCES: 37
CORRESPONDENCE ADDRESS:
GENERAL INFORMATION:
APPLICANT: Innis, Michael
APPLICANT: Creasey, Abla
TITLE OF INVENTION: Chimeric Proteins
NUMBER OF SEQUENCES: 37
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                 FILING DATE: 09-MAY-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/286,521
FILING DATE: 05-AUG-1994
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: US/08/436,175
FILING DATE: 09-MAY-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0990.001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Chiron Corporation
                                                                                                                                    Chiron Corporation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME: Savereide Paul B.
REGIESTRATION NUMBER: 36,914
REFERENCE/DOCKET NUMBER: 09
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          INFORMATION FOR SEQ ID NO: 19: SEQUENCE CHARACTERISTICS: LENGTH: 161 amino acids TYPE: amino acid STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 : 510-601-2585
510-655-3542
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ADDRESSEE: Chiron Corpo
STREET: 4560 Horton St
CITY: Emeryville
                                                                                                                                                      4560 Horton St
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Matches 161; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TOPOLOGY: linear MOLECULE TYPE: peptide
                                                                                                                                                      STREET: 4560 HOLUCITY: Emeryville
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity
                                                                                                                                                                                                                         USA
                                                                                                                                                                                                                                         94608
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    94608
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEPHONE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CA
                                                                                                                                                                                                       S
                                                                                                                                  ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 4
US-08-943-682-19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-08-436-175-19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COUNTRY:
                                                                                                                                                                                                                         COUNTRY:
                                                                                                                                                                                                   STATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STATE:
```

ó

```
g
                                                                                                                                                                                                                                                                                                                                                                                                                              δλ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ŏ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              61 GNQNRFESLEECKKMCTRDNANRIIKTTLQQEKPDFCFLEEDPGICRGYITRYFYNQQTK 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 DSEEDEEHTIITDTELPPLKLMHSFCAFKADDGPCRAIMKRFFFNIFTRQCEEFIYGGCE 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 161;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
            MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
COMPOTER: IBM PC COMPATIBLE
CORPATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30B
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/943,682
FILING DATE: 03-0CT-1997
CLASSIFICATION NUMBER: US 08/438,184
FILING DATE: 09-MAY-1995
APPLICATION NUMBER: US 08/286,521
FILING DATE: 05-AUG-1994
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ZIP: 94608
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30B
APPLICATION NUMBER: PCT/US95/09464
FILING DATE: Z5-JULY-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                121 QCERFKYGGCLGNMNNFETLEECKNICEDGPNGFQVDNYGT 161
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         121 QCERFKYGGCLGNMNNFETLEECKNICEDGPNGFQVDNYGT 161
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 100.0%; Score 905; DB 4; Best Local Similarity 100.0%; Pred. No. 1.1e-92;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 19, Application PC/TUS9509464
GENERAL INFORMATION:
APPLICANT: CHIRON CORPORATION
TILLE OF INVENTION: Chimeric Proteins
NUMBER OF SEQUENCES: 37
CORRESPONDENCE ADDRESS:
ADDRESSE: Chiron Corporation
STREET: 4560 Horton St.
                                                                                                                                                                                                                                                                                                                                              0990.001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Savereide, Paul B.
REJISTRATION NUMBER: 36,914
                                                                                                                                                                                                                                                                                                  NAME: Savereide, Paul B.
REGISTRATION NUMBER: 36,914
REFERENCE/DOCKET NUMBER: 099
                                                                                                                                                                                                                                                                                                                                                               TELECOMMUNICATION INFORMATION: TELEPHONE: 510-601-2585
                                                                                                                                                                                                                                                                                                                                                                                  TELEPHONE: 510-601-2585
TELEFAX: 510-655-3542
INFORMATION FOR SEQ ID NO: 19:
                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE CHARACTERISTICS:
LENGTH: 161 amino acids
TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Matches 161; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; MOLECULE TYPE: peptide US-08-943-682-19
COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 5
PCT-US95-09464-19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CITY: STATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         δλ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ò
```

```
ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      61 GNONRFESLEECKKMCTRDNANRIIKTTLQQEKPDFCFLEEDPGICRGYITRYFYNQQTK 120
                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                1 DSEEDEEHTIITDTELPPLKLMHSFCAFKADDGPCRAIMKRFFFNIFTRQCEEFIYGGCE 60
                                                                                                                                                                                                                                                                                                                                                                         1 DSEEDEEHTIITDTELPPLKLMHSFCAFKADDGPCRAIMKRFFFNIFTRQCEEFIYGGCE 60
                                                                                                                                                                                                                                                                                                                                  ö
                                                                                                                                                                                                                                                                                  Length 161;
                                                                                                                                                                                                                                                                                                                                0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SOFTWARE: PatentIn Release #1.0, Version #1.30B CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/437,841
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      121 QCERFKYGGCLGNMNNFETLEECKNICEDGPNGFQVDNYGT 161
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             121 QCERFKYGGCLGNMNNFETLEECKNICEDGPNGFQVDNYGT 161
                                                                                                                                                                                                                                                                                100.0%; Score 905; DB 5;
100.0%; Pred. No. 1.1e-92;
tive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-016.437-841-9
Sequence 9, Application US/08437841
Patent No. 5563123
GENERAL INFORMATION:
APPLICANT: Innis, Michael
APPLICANT: Creasey, Abla
TITLE OF INVENTION: Chimeric Proteins
NUMBER OF SEQUENCES: 37
CORRESPONDENCE ADDRESS:
ADDRESSEE: Chiron Corporation
STREET: 4560 Horton St.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME: Savereide, Paul B.
REGISTRATION NUMBER: 36,914
REFERENCE/DOCKET NUMBER: 0990.001
REFERENCE/DOCKET NUMBER: 0990.100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/286,521
FILING DATE: 05-AUG-1994
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
             TELECOMMUNICATION INFORMATION:
TELEPHONE: 510-601-2585
TELEPAX: 510-655-3542
INFORMATION FOR SEQ ID NO: 19:
SEQUENCE CHARACTERISTICS:
LENGTH: 161 amino acids
TYPE: amino acids
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELECOMMUNICATION INFORMATION:
TELEPHONE: 510-601-2585
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         276 amino acids
                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity 100.0
Matches 161; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEFAX: 510-655-3542 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE CHARACTERISTICS
                                                                                                                                                                                           TOPOLOGY: linear
MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-437-841-9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ZIP: 94608
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       S
                                                                                                                                                                                                                                         PCT-US95-09464-19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STATE:
```

us-09-741-106-19.rai

121 QCERFKYGGCLGNMNNFETLEECKNICEDGPNGFQVDNYGT 161

g

```
ö
                                        ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     61 GNQNRFESLEECKKMCTRDNANRIIKTTLQQEKPDFCFLEEDPGICRGYITRYFYNQQTK 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          61 GNONRFESLEECKKMCTRDNANRIKTTLQQEKPDFCFLEEDPGICRGYITRYFYNNQTK 120
                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 DSEEDEEHTIITDTELPPLKLMHSFCAFKADDGPCRAIMKRFFFNIFTRQCEEFIYGGCE 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 DSEEDEEHTIITDIELPPLKLMHSFCAFKADDGPCRAIMKRFFFNIFITRQCEEFIYGGCE 60
                                                                                                 Gaps
                                                                             1 DSEEDEEHTIITDIELPPLKLMHSFCAFKADDGPCRAIMKRFFFNIFTRQCEEFIYGGCE 60
                                      ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           99.4%; Score 900; DB 1; Length 276; 99.4%; Pred. No. 7.7e-92; ive 0; Mismatches 1; Indels
Score 900; DB 1; Length 276;
Pred. No. 7.7e-92;
0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SOFTWARE: Patentin Release #1.0, Version #1.30B CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   121 QCERFKYGGCLGNMNNFETLEECKNICEDGPNGFQVDNYGT 161
                                                                                                                                                                                                                                                          121 QCERFKYGGCLGNMNNFFTLEECKNICEDGPNGFQVDNYGT 161
                                                                                                                                                                                                                                        121 OCERFKYGGCLGNMNNFETLEECKNICEDGPNGFQVDNYGT 161
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Innis, Michael
APPLICANT: Creasey, Abla
TITLE OF INVENTION: Chimeric Proteins
NUMBER OF SEQUENCES: 37
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ATTORNEY/AGENT INFORMATION:
NAME: Saverelde, Paul B.
REGISTRATION NUMBER: 36,914
REFERENCE/DOCKET NUMBER: 0990.001
TELECOMUNICATION INFORMATION:
TELEDHONE: 510-661-2585
TELEFAX: 510-655-3542
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: US/08/286,521
FILING DATE: 05-AUG-1994
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Chiron Corporation
                                                                                                                                                                                                                                                                                                                                                       US-08-286-521-9; Sequence 9, Application US/08286521; Sequence No. 5589359; CALENT NO. 5689359; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              INFORMATION FOR SEQ ID NO: 9: SEQUENCE CHARACTERISTICS: LENGTH: 276 amino acids
99.48;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   4560 Horton St
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Matches 160; Conservative
                                        Matches 160; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Emeryville
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: amino acid
                      Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  94608
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STATE: CA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US-08-286-521-9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STREET:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
    Query Match
                        Best Local
                                                                                                                                                                                                                                                                                                                                         RESULT 7
                                                                                                                                                            δ
                                                                                                                                                                                                 qq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            P
                                                                                                                                                                                                                                          ð
```

```
61 GNQNRFESLEECKKMCTRDNANRIIKTTLQQEKPDFCFLEEDPGICRGYITRYFYNQQTK 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                61 GNONRFESLEECKKMCTRDNANRIKTTLQQEKPDFCFLEEDPGICKGYITRYFYNNQTK 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 DSEEDEEHTIITDTELPPLKLMHSFCAFKADDGPCRAIMKRFFFUIFTRQCEEFIYGGCE 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 DSEEDEEHTIITDTELPPLKLMHSFCAFKADDGPCRAIMKRFFFNIFTRQCEEFIYGGCE 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Ouery Match

99.4%; Score 900; DB 1; Length 276;
Best Local Similarity 99.4%; Pred. No. 7.7e-92;
Matches 160; Conservative 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 3, Application US/08854764
Patent No. 6103500
GENERAL INFORMATION:
APPLICANT: Innes, Michael
APPLICANT: Lores, Abla
TITLE OF INVENTION: Production of Tissue Factor Pathway
TITLE OF INVENTION: Inhibitor
                                                                                                                                                                                                                                                                                                                                                                                                                                                             SOFTWARE: Patentin Release #1.0, Version #1.30B CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       121 QCERFKYGGCLGNMNNFETLEECKNICEDGPNGFQVDNYGT 161
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              121 QCEREKYGGCLGNMNNFETLEECKNICEDGPNGFQVDNYGT 161
                                                                                         APPLICANT: Innis, Michael
APPLICANT: Creasey, Abla
TITLE OF INVENTION: Chimeric Proteins
NUMBER OF SEQUENCES: 37
CORRESPONDENCE ADDRESS:
ADDRESSEE: Chiron Corporation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FILING DATE: 09-MAY-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/286,521
FILING DATE: 05-AUG-1994
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: US/08/436,175
FILING DATE: 09-MAY-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0990.001
                                                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERAIING SYSTEM: PC-DOS/MS-DOS
               Sequence 9, Application US/08436175 Patent No. 5696088
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 REFERENCE/DOCKET NUMBER: 09
TELECOMMUNICATION INFORMATION:
TELEPHONE: 510-601-2585
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME: Savereide, Paul B. REGISTRATION NUMBER: 36,914
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEPHONE: 510-601-2585
TELEFAX: 510-655-3542
INFORMATION FOR SEQ ID NO: 9:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE CHARACTERISTICS:
LENGTH: 276 amino acids
                                                                                                                                                                                                                                          STREET: 4560 Horton St
CITY: Emeryville
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              amino acid
                                                                         GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                      USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                           94608
                                                                                                                                                                                                                                                                                                  CA
                                                                                                                                                                                                                                                                                                                      COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT 9
US-08-854-764-3
US-08-436-175-9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-08-436-175-9
                                                                                                                                                                                                                                                                      CITY: E
STATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          δλ
```

ö

```
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                      TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-08-943-682-9
                                                                                                                                                                                                                                                                                                                                                                                         LENGIH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ŏ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                61 GNONRFESLEECKKMCTRDNANRIIKTTLQQEKPDFCFLEEDPGICRGYITRYFYNQQTK 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      61 GNONRFESLEECKKMCTRDNANRIKTTLQQEKPDFCFLEEDPGICKGYITRYFYNNQTK 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 DSEEDEEHTIITDTELPPLKLMHSFCAFKADDGPCRAIMKRFFFNIFTRQCEEFIYGGCE 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 DSEEDEEHTIITDTELPPLKLMHSFCAFKADDGPCRAIMKRFFFNIFTRQCEFFIYGGCE 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              99.4%; Score 900; DB 3; Length 276; 99.4%; Pred. No. 7.7e-92;
                                                                                                                                                                                                 UPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.30B
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/854,764
FILING DATE: 12-MAY-1997
CLASSIFITAMENT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   121 QCERFKYGGCLGNMNNFETLEECKNICEDGPNGFQVDNYGT 161
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         121 QCERFKYGGCLGNMNNFETLEECKNICEDGPNGFQVDNYGT 161
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                          NAME: Savereide, Paul B.
REGISTRATION NUMBER: 36,914
REFERENCE/DOCKET NUMBER: 0991.001
TELECOMMUNICATION INFORMATION:
TELEPHONE: 510-61-2585
INFORMATION FOR SEQ. ID NO: 3:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Innis, Michael
APPLICANT: Creasey, Abla
TITLE OF INVENTION: Chimeric Proteins
NUMBER OF SEQUENCES: 37
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                       FILING DATE: 12-MAY-1997
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/286,530
FILING DATE: 05-AUG-1994
ATTORNEY,AGENT INFORMATION:
NAME: Savereide, Paul B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ZIP: 94608
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ADDRESSEE: Chiron Corporation
STREET: 4560 Horton St.
CITY: Emeryville
STATE: CA
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 9, Application US/08943682
Patent No. 6174721
GENERAL INFORMATION:
                 CORRESPONDENCE ADDRESS:
ADDRESSEE: Chiron Corporation
                                                                                                                                                            COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LENGTH: 276 amino acids TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity 99.44
Matches 160; Conservative
                                                      STREET: 4560 Horton St
CITY: Emeryville
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TOPOLOGY: linear; MOLECULE TYPE: peptide US-08-854-764-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              single
NUMBER OF SEQUENCES: 7
                                                                                        CA
USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STRANDEDNESS:
                                                                                                                                        94608
                                                                                                 STATE: CA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-08-943-682-9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          qq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   δ
```

```
61 GNONRFESLEECKKMCTRDNANRIIKTTLOQEKPDFCFLEEDPGICRGYITRYFYNQQTK 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 DSEEDEEHTIITDTELPPLKLMHSFCAFKADDGPCRAIMKRFFFNIFTRQCEEFIYGGCE 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 DSEEDEEHTIITDTELPPLKLMHSFCAFKADDGPCRAIMKRFFFNIFTRQCEEFIYGGCE 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          99.4%; Score 900; DB 4; Length 276; 99.4%; Pred. No. 7.7e-92; tive 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT 11
PCT-US95-09377-3
Sequence 3, Application PC/TUS9509377
GENERAL INFORMATION:
THILE OF INVENTION: Production of Tissue Factor Pathway
TITLE OF INVENTION: Inhibitor
UNMBER OF SEQUENCES: 7
CORRESPONDENCE ADDRESS: ADDRESS: ADDRESS: ADDRESSEE: Chiron Corporation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDIUM TYPE: Floppy disk
COMBUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30B
CURRENT APPLICATION DATA:
SOFTWARE: Patentin Release #1.0, Version #1.30B CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/943,682
FILING DATE: 03-00T-1997
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             121 QCERFKYGGCLGNMNNFETLEECKNICEDGPNGFQVDNYGT 161
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CLASSIPLICATION: 43.0

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/438,184
FILING DATE: 09-MA-1993
APPLICATION NUMBER: US 08/286,521
FILING DATE: 05-AUG-1994
ATTORNEY/AGENT INFORMATION:
NAME: Savereide, Paul B.
REGISTRATION NUMBER: 36,914
REFERENCE/DOCKET NUMBER: 36,914
TELECHONE: 510-601.2585
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PCI/US95/09377
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ATTORNEY/AGENT INFORMATION:
NAME: Savereide, Paul B.
REGISTRATION NUMBER: 36,914
REFERENE/DOCKET NUMBER: 0991.100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELECOMMUNICATION INFORMATION:
TELEPHONE: 510-601-2585
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          25-JULY-1995
                                                                                                                                                                                                                                                                                                                                                          TELEFAX: 510-655-3542
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                            276 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Best Local Similarity 99.4
Matches 160; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ZIP: 94608
COMPUTER REDABLE FORM:
MEDIUM TYPE: Flore:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Emeryville
                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: amino acid
STRANDEDNESS: sir
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          linear
```

ó

```
NAME/KEY: Active-site LOCATION: 228..229
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: amino acid
STRANDEDNESS: si
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       linear
                                                                                                                                                                                                                                                         GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                    STATE: Georgia
COUNTRY: U.S.A.
ZIP: 30303
                                                                                                                                                                                                                                                                                                                                                                                                                CITY: Atlanta
STATE: Georgia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ANTI-SENSE: NO FRAGMENT TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         HYPOTHETICAL:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SOFTWARE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LOCATION:
                                                                                                                                                                                 RESULT 13
US-08-796-850-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FEATURE:
                                                      q
                                                                                            ŏ
                                                                                                                              q
                                                                                                                                                                                                                     ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0
                                                                                                                                                                                                                                                                                                                                        61 GNQNRFESLEECKKMCTRDNANRIKTTLQQEKPDFCFLEEDPGICKGYITRYFYNNQTK 120
                                                                                                                                                                                                                                                                                                                       61 GNQNRFESLEECKKMCTRDNANRIIKTTLQQEKPDFCFLEEDPGICRGYITRYFYNQQTK 120
                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                 1 DSEEDEEHTIITDTELPPLKLMHSFCAFKADDGPCRAIMKRFFFNIFTRQCEEFIYGGCE 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 DSEEDEEHTIITDTELPPLKLMHSFCAFKADDGPCRAIMKRFFFNIFTRQCEEFIYGGCE 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ;
0
                                                                                                                                                                           99.4%; Score 900; DB 5; Length 276; 99.4%; Pred. No. 7.7e-92; tive 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           99.4%; Score 900; DB 5; Length 276; 99.4%; Pred. No. 7.7e-92; Live 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPOUTER READBLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30B
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/09464
FILING DATE: 25-JULY-1995
                                                                                                                                                                                                                                                                                                                                                                                           121 QCERFKYGGCLGNMNNFETLEECKNICEDGPNGFQVDNYGT 161
                                                                                                                                                                                                                                                                                                                                                                                                              121 QCERFKYGGCLGNMNNFETLEECKNICEDGPNGFQVDNYGT 161
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 9, Application PC/TUS9509464
GENERAL INFORMATION:
APPLICANT: CHIRON CORPORATION
TITLE OF INVENTION: Chimeric Proteins
NUMBER OF SEQUENCES: 37
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Savereide, Paul B.
REGISTRATION NUMBER: 36,914
REPERBRENG-ZPOCKET NUMBER: 0990.100
TELECOMMUNICATION INFORMATION:
TELEPHONE: 510-601-25885
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ADDRESSEE: Chiron Corporation STREET: 4560 Horton St.
           INFORMATION FOR SEQ ID NO: 3
SEQUENCE CHARACTERISTICS:
LENGTH: 276 amino acid
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEFAX: 510-655-3542
INFORMATION FOR SEQ ID NO: 9
SEQUENCE CHARACTERISTICS:
LENGTH: 276 amino acids
                                                                                                                                                                                                               Matches 160; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Best Local Similarity 99.49
Matches 160; Conservative
TELEFAX: 510-655-3542
                                                                                 STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                    TOPOLOGY: linear MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MOLECULE TYPE: peptide
                                                                                                                                                                                                Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Emeryville
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STATE: CA COUNTRY: US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT 12
PCT-US95-09464-9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TOPOLOGY:
                                                                                                                                         PCT-US95-09377-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PCT-US95-09464-9
                                                                                                                                                                             Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
                                                                                                                                                                                                                                                                                   q
                                                                                                                                                                                                                                                                                                                                                     g
                                                                                                                                                                                                                                                                                                                         ò
                                                                                                                                                                                                                                                                                                                                                                                           δ
                                                                                                                                                                                                                                                                                                                                                                                                                             g
```

```
61 GNONRFESLEECKKMCTRDNANRIIKTTLQQEKPDFCFLEEDPGICRGYITRYFYNNQTK 120
61 GNQNRFESLEECKKMCTRDNANRIIKTTLQQEKPDFCFLEEDPGICRGYITRYFYNQQTK 120
                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Papathanassiu, Adonia E
APPLICANT: Papathanassiu, Adonia E
TITLE OF INVENTION: Compositions and Methods for Inhibiting
TITLE OF INVENTION: Cellular Proliferation
NUMBER OF SEQUENCES: 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LOCATION: 117..118
OTHER INFORMATION: /note= "Potential site for N-linked OTHER INFORMATION: glycosylation"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LOCATION: 167..168
OTHER INFORMATION: /note= "Potential site for N-linked OTHER INFORMATION: glycosylation"
                                                                                                                                  121 QCERFKYGGCLGNMNNFETLEECKNICEDGPNGFQVDNYGT 161
                                                                                                       121 QCERFKYGGCLGNMNNFETLEECKNICEDGPNGFQVDNYGT 161
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Patentin Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                OTHER INFORMATION: /note= "Site of partial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CORRESPONDENCE ADDRESS:
ADDRESSEE: Jones & Askew
STREET: 191 Peachtree Street, 37th Floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             05213-0290
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 OTHER INFORMATION: phosphorylation"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/796,850
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                    ; Sequence 1, Application US/08796850 ; Patent No. 5981471
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   REFERENCE/DOCKET NUMBER: 0521:
TELECOMUNICATION INCORMATION:
TELEPHONE: (404) 818-3700
TELEFAX: (404) 818-3799
INPORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 276 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             32,467
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ATTORNEY/AGENT INFORMATION:
NAME: Greene, Jamie L.
REGISTRATION NUMBER: 32,4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                N-terminal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME/KEY: Active-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME/KEY: Active-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME/KEY: Active-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MOLECULE TYPE: protein HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CLASSIFICATION: 514
```

```
.;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   61 GNONRFESLEECKKMCTRDNANRIIKTTLQQEKPDFCFLEEDPGICRGYITRYFYNQQTK 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         61 GNONRFESLEECKKMCTRDNANRIKTTLQQEKPDFCFLEEDPGICRGYITRYFYNNQTK 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 DSEEDEEHTIITDTELPPLKIMHSFCAFKADDGPCKAIMKRFFFNIFTRQCEEFIYGGCE 60
                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 DSEEDEEHTIITDTELPPLKLMHSFCAFKADDGPCRAIMKRFFFNIFTRQCEFIYGGCE 60
                                                                                                                                                                                                                                                                                                                                                                                                                        ;
0
                                                                                                                                                                                                                                                                                                                                                                        / Match 99.1%; Score 897; DB 2; Length 276; Local Similarity 98.8%; Pred. No. 1.7e-91; nes 159; Conservative 1; Mismatches 1; Indels
/note= "Potential site for N-linked
glycosylation"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Diaz-Collier, Judy A.
APPLICANT: Gustafson, Mark E.
APPLICANT: Win, Tze-Chein
TITLE OF INVENTION: Method of Producing Tissue Factor
TITLE OF INVENTION: Pathway Inhibitor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          121 QCERFKYGGCLGNMNNFETLEECKNICEDGPNGFQVDNYGT 161
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     121 QCERFKYGGCLGNMNNFETLEECKNICEDGPNGFQVDNYGT 161
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ADDRESSEE: Scott J. Meyer, Monsanto Co., A3SG
STREET: 800 N. Lindbergh Blvd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ATTORNEY/AGENT INFORMATION:
NAME: Meyer, Scott J.
REGISTRATION NUMBER: 25,275
REFERENCE/DOCKET NUMBER: 07-21(819)A
TELECOMMUNICATION INFORMATION:
TELEPHONE: (314)694-3117
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                              LOCATION: 189..239
CTHER INFORMATION: /label= Kunitz-3
US-08-796-850-1
                                                                                                                                                                                                              /label= Kunitz-2
                                                                                                                  /label= Kunitz-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: US/07/844,297
FILING DATE: 19920302
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 1, Application US/07844297
Patent No. 5212091
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      : 277 amino acids
AMINO ACID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; MOLECULE TYPE: protein US-07-844-297-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
COMPUTER: IBM PC COM
                                                                 NAME/KEY: Domain
LOCATION: 26..76
OTHER INFORMATION:
                                                                                                                                                                                    LOCATION: 97..147 OTHER INFORMATION:
OTHER INFORMATION: OTHER INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      linear
                                                                                                                                                                                                                                                          NAME/KEY: Domain
                                                                                                                                                                NAME/KEY: Domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CITY: St. Louis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STATE: Missouri
COUNTRY: U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FILING DATE: 19
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        63167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LENGIH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-07-844-297-1
                                                                                                                                                                                                                                                                                                                                                                               Query Match
                                                                                                                                                                                                                                                                                                                                                                                                     Best Loca
Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               рp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             οy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                δ
```

```
ö
                                            ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
ADDRESSEE: No. 53786140 No. 5378614disk of No. 5378614th America, Inc.
                                                                                                                                                                                                      62 GNONRFESLEECKKMCTRDNANRIIKTTLQQEKPDFCFLEEDPGICRGYITRYFYNNQTK 121
                                                                                                                                                                               61 GNONRFESLEECKKMCTRDNANRIIKTTLQQEKPDFCFLEEDPGICRGYITRYFYNQQTK 120
                                                                                        1 DSEEDEEHTIITDTELPPLKLMHSFCAFKADDGPCRAIMKRFFFNIFTRQCEFFIYGGCE 60
                                                                                                                  2 DSEEDEEHTIITDTELPPLKLMHSFCAFKADDGPCKAIMKRFFFNIFTRQCEEFIYGGCE 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 DSEEDEEHTIITDTELPPLKLMHSFCAFKADDGPCRAIMKRFFFNIFTRQCEEFIYGGCE 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
                                              ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 99.1%; Score 897; DB 1; Length 304; Best Local Similarity 98.8%; Pred. No. 1.9e-91; Matches 159; Conservative 1; Mismatches 1; Indels
Score 897; DB 1; Length 277; Pred. No. 1.7e-91;
                                            Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GENERAL INFORMATION:
APPLICANT: Petersen, Jens G. Litske
APPLICANT: No. 5378614dfang, Ole Juul
TITLE OF INVENTION: Method for Making TFPI Analogues
                                                                                                                                                                                                                                                                   SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/026,145
FILING DATE: 19930302
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: WO PCT/DK/90/00212
FILING DATE: 17-AUG-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: DK 4080/89
FILING DATE: 18-AUG-1989
ATTORNEY/AGENT INFORMATION:
NAME: AGTIS, Cherryl H.
REGISTRATION NUMBER: 34086
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STREET: 405 Lexington Avenue, Suite 6200 CITY: New York
                                              1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRIOR APPLICATION: 4.55
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/828,920
FILING DATE: 27-0AN-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO PCT/DK/90/0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             : N. Y.
RY: United States of America
10174-6201
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 2, Application US/08026145 Patent No. 5378614
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   REFERENCE/DOCKET NUMBER: 33
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212 867 0123
TELEFAX: 212 867 0298
99.1%;
98.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEFAX: 212 867 0298
INFORMATION FOR SEQ ID NO: 2:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             304 amino acids
                                              Matches 159; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; MOLECULE TYPE: protein US-08-026-145-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: AMINO ACID TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FILING DATE: 199
CLASSIFICATION:
                         Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                            US-08-026-145-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STATE:
    Query Match
                                                                                                                                                                                                                                                                                                                                                                                   RESULT 15
                                                                                             ΟŻ
                                                                                                                                  Db
                                                                                                                                                                               ò
                                                                                                                                                                                                                           g
                                                                                                                                                                                                                                                                       δy
                                                                                                                                                                                                                                                                                                               q
```

- 29 DSEEDEEHTIITDTELPPLKLMHSFCAFKADDGPCKAIMKRFFFNIFTRQCEEFIYGGCE 88 g
- O.Y D.b
- - Qy Db

Search completed: December 2, 2002, 10:05:59 Job time: 27.4328 secs

```
GenCore version 5.1.3
Copyright (c) 1993 - 2002 Compugen Ltd.
```

OM protein - protein search, using sw model

December 2, 2002, 10:00:35 ; Search time 28.8358 Seconds Run on:

(without alignments) 536.751 Million cell updates/sec

US-09-741-106-19

1 DSEEDEEHTIITDTELPPLK......ECKNICEDGPNGFQVDNYGT 16: Perfect score: Sednence:

Scoring table:

BLOSUM62 Gapop 10.0 , Gapext 0.5

Total number of hits satisfying chosen parameters:

283224 segs, 96134422 residues

Searched:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

PIR\_73:\* Database :

1: pir1:\* 2: pir2:\* 3: pir3:\* 4: pir4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	tissue factor path	factor	otein-as	tissue factor path		tissue factor path		m	hypothetical prote		_	_	4	Q	_	hepatocyte growth	hypothetical prote	protein ZC84.6 [im	alpha-1-microglobu	protein T22F7.3 [i	hypothetical prote	hypothetical prote	alpha-1-microglobu	alpha-1-microglobu	inter-alpha-trypsi	alpha-1-microglobu	alpha-1-microglobu	hypothetical prote		
SUMMARIES	ID	$\mathbf{H}$	JC2264	S12143	146937	TIRTGK	S53325	A54951	8	T34395	T26063	T20125	T23573	E88550	S28291	T16210	JG0185	T33216	D88550	TIBOBI	н88380	T21275	T26859	TIPGBI	S35708	A29652	TIHOBI	S21089	04	T19734	
	DB	П	7	N	7	7	~	7	7	7	7	7	ď	~1	7	7	7	7	7	٦	ď	~	7	Н	~	7	Н	7	7	∾.	
	Length	304	304	300	299	302	386	235	1558	2167	2225	838	922	1416	2844	1599	252	1965	1474	352	1522	1203	1743	337	349	123	125	349	1391	1043	
æ	Query	99.1	92.4	72.2	71.3	9.59	8.09	30.3	29.4	29.4	28.5	27.8	27.0	26.7	26.7	26.6	26.3	26.3	26.0	25.8	25.7	25.0	24.4	24.4	24.0	23.9	23.4	23.2	22.8	22.4	
	Score	897	836	653	645	594	550	274.5	266.5	266.5	257.5	252	244	241.5	241.5	240.5	238	238	235	233.5	233	226.5	221	220.5	217	216.5	211.5	$\overline{}$	206.5	0	
	Result No.	н	7	æ	4	5	9	7	80	σ	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	29	

alpha-1-microglobu	gamma-1-microglobu	hypothetical prote	venom basic protei	hypothetical prote	venom basic protei	venom basic protei	taicatoxin serine	hypothetical prote	basic proteinase i	hypothetical prote	trypsin inhibitor,	venom basic protei	alpha-1-microglobu	venom basic protei	proteinase inhibit
нсно	S22181	T28711	TIVIVC	T34212	S19327	TIVIT1	A44180	T27822	TITTOR	T32980	TIBOC	TIVRV2	JC2556	TIRIV2	S07451
Н	-	7	Н	7	7	-	7	7	Н	7	П	7	7	П	7
352	355	183	65	802	62	61	62	1208	110	692	67	9	372	57	62
22.0	21.3	21.0	21.0	20.9	20.3	20.1	19.6	19.2	19.0	19.0	18.9	18.8	18.7	18.5	18.5
199.5	192.5	190.5	190	189.5	184	182	177	173.5	172	171.5	171	170	169.5	167	167
0		2	e	4	Ŋ	ب	7	œ	6	0	_	7	æ	4	S

### ALIGNMENTS

tissue factor pathway inhibitor precursor [validated] - human
N.Alternate names: extrinsic pathway inhibitor; lipoprotein-associated coagulation in
C.Species: Homo sapiens (man)
C.Date: Homo sapiens (man)
C.Date: 30-Jun-1992 #sequence\_revision 30-Jun-1992 #text\_change 08-Dec-2000
C.Date: 30-Jun-1992 #sequence\_revision 30-Jun-1992 #text\_change 08-Dec-2000
C.Date: 30-Jun-1992 #sequence\_revision 30-Jun-1992 #text\_change 08-Dec-2000
C.Date: 30-Jun-1992 #sequence\_revision 30-Jun-1993; Bi0433; S13034; A34315; A38234; S03903
R.Girard, T.J.; Eddy, R.; Wesselschmidt, R.L.; MacPhail, L.A.; Likert, K.M.; Byers, M.J. tille: Structure of the human lipoprotein-associated coagulation inhibitor gene. In
A.Reference number: A23712; MUID:91161593; PMID:2002045

A Molecule type: DNA
A, Residues: 1-304 «GIR»
A, Residues: 1-304 «GIR»
A, Cross-references: GB:M59493; GB:M59499; NID:g187204; PIDN:AAA59526.1; PID:g187206
A, Cross-references: GB:M59493; GB:M59499; NID:g187204; PIDN:AAA59526.1; PID:g187206
B, van der Logt, C.P.E.; Reitsma, P.H.; Bertina, R.M.
Bjochemistry 30, 1571-11577, 1991
A; Title: Intron-exon organization of the human gene coding for the lipoprotein-associal A; Reference number: A39176; MUID:91129227; PMID:1993173

A; Accession: A39176

A; Molecule type: DNA A; Residues: 1-304 </ANA A; Residues: 1-304 </ANA A; Cross-references: GB:M58650; GB:J05312; NID:g186827; PIDN:AAA59480.1; PID:g186829 R; Wun, T.C.; Kretzmer, K.K.; Girard, T.J.; Miletich, J.P.; Broze Jr., G.J. J. Biol. Chem. 253, 6001-6004, 1988 A; Title: Cloning and characterization of a cDNA coding for the lipoprotein-associated A; Reference number: A28650; MUID:88198127; PMID:2452157

A.Molecule type: mRNA
A.Residues: 1-304 <WUN>
A.Residues: 1-304 <WUN>
A.CREST references: GB3.03225; NID:g180545; PIDN:AAA52022.1; PID:g180546
A.Cross-references: GB3.03225; NID:g180545; PIDN:AAA52022.1; PID:g180546
A.Cross-references of B3.003225; NID:g180545; Bejoek, B.E.; Miletich, J.P.; Broze Jr., Thromb. Res. 55, 37-50, 1989
A.Title: Identification of the 1.4 KB and 4.0 KB messages for the lipoprotein associa A.Reference number: A60433; MUID:89388722; PMID:2781520

A; Status: not compared with conceptual translation

A; Molecule type: mRNA A; Residues: 1-304 <GI

A; Residues: 1-304 <G12> A; Experimental source: endothelial cells A; Accession: B60433

A; Molecule type: protein
A; Residues: 'Xx',31-53,'Xx',55-56 <G13>
A; Residues: 'Xx',31-53,'Xx',55-56 <G13>
A; Experimental Source: recombinant material from mouse C137 cells
B; Grard, T.J.; McCourt, D.; Novotny, W.F.; MacPhail, L.A.; Likert, K.M.; Broze Jr.,
Biochem. J. 270, 621-625, 1990
A; Title: Endogenous phosphorylation of the lipoprotein-associated coagulation inhibit
A; Reference number: \$13034; MUID:91054349; PMID:2122883

A; Molecule type: protein A; Residues: 29-35 <GI4>

```
NONRFESLEECKKMCTRDNANRIIKTTLQQEKPDFCFLEEDPGICRGYITRYFYNQQTKQ 121
                            A; Molecule type: mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   149
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ōλ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Вb
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      qq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Óλ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      δ
R:Novotny, W.F.; Girard, T.J.; Miletich, J.P.; Broze Jr., G.J.
J. BAOJ. Chem. 264, 18832,18937, 1899
A.Tille: Purification and characterization of the lipoprotein-associated coagulation inf
A.Recession: A4315
A.Accession: A4315
A.Accession: A4315
A.Accession: A4315
A.Residues: Yax.,31-33, T.,35-50 «NOV)
A.Residues: Yax.,31-33, T.,35-50 «NOV)
A.Residues: Yax.,31-33, T.,35-50 «NOV)
A.Residues: A.H.; Nordiagy O.; Nortis, F.; Wiberg, F.C.; Christensen, P.M.; Moeller, K.
A.Recensentantal source: plasm
B.Pedersen, A.H.; Nordiagy O.; Nortis, F.; Wiberg, F.C.; Christensen, P.M.; Moeller, K.
A.Tille: Recombinant human extrinsic pathway inhibitor. Production, isolation, and characteristic protein was extrinsic pathway inhibitor.
A.Reference numbers. A38294; MUID:91009092; PMID:2211593
A.Accession: A38204
A.M. Reliance of the Kunitz-type inhibitory domains of lipoprotein-assample in the coagulation of size directed musageness the factor VIIa/tissue factor complex; the Comment. The first Kunitz-type domain binds the factor VIIa/tissue factor complex; the Comment. The first Kunitz-type domain binds the factor VIIa/tissue factor complex; the Comment. The first Kunitz-type domain binds the factor VIIa/tissue factor complex; the Comment. The first Kunitz-type proteinse inhibitot of the coagulation of Superfamily: tissue factor pathway inhibitor; animal Kunitz-type proteinse inhibitor homology 48P2>
F. 217-28/Domain: signal sequence fattus predicted 4510
C. Kewpords: anticoagulant, Diod coagulation fattus experimental can man kunitz-type proteinse inhibitor homology 48P2>
F. 217-28/Domain: animal kunitz-type protei
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  National factor pathway inhibitor precursor - rhesus macaque
Naternate names: extrinsic pathway inhibitor; lipoprotein-associated coagulation inhib
Naternate names: extrinsic pathway inhibitor; lipoprotein-associated coagulation inhib
S. Specias: Macaca mulatta (rhesus macaque)
C. Date: 10.5ep-1999 #sequence_revision 10.5ep-1999 #text_change 21-Jul-2000
C. Accession: JC2264
N. Ramel, S.; Kamklubo, Y.; Hamuro, T.; Fujimoto, H.; Ishihara, M.; Yonemura, H.; Miyamot
A;Title: Amino acid sequence and inhibitory activity of rhesus monkey tissue factor path
A;Reference number: JC2264; MUID:94375417; PMID:8089087
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GNONRFESLEECKKMCTRDNANRIIKTTLQQEKPDFCFLEEDPGICRGYITRYFYNQQTK 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             29 DSEEDEEHTIITDTELPPLKLMHSFCAFKADDGPCKAIMKRFFFNIFTRQCEEFIYGGCE 88
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 DSEEDEEHTIITDTELPPLKLMHSFCAFKADDGPCRAIMKRFFFNIFTROCEEFIYGGCE 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 304;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               99.1%; Score 897; DB 1; Lengtn 505.08 8%; Pred. No. 1.3e-76;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   121 QCERFKYGGCLGNMNNFETLEECKNICEDGPNGFQVDNYGT 161
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           149 QCERFKYGGCLGNMNNFETLEECKNICEDGPNGFQVDNYGT 189
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ŏ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   δ
```

```
NyAlternate names: endothelial cell coaquiation precuisor. Idabbit.

NyAlternate names: endothelial cell coaquiation inhibitor; endothelial cell tissue fa C; Species: Oryctolagus cuniculus (domestic rabbit)

C; Species: Oryctolagus cuniculus (domestic rabbit)

C; Sacession: 512143; A61373

R; Wesselschmidt, R.L.; Girard T.J.; Broze Jr., G.J.

Nucleic Acids Res. 18, 6440, 1990

A; Title: CDNA sequence of rabbit lipoprotein associated coagulation inhibitor.

A; Reference number: S12143; MUID:91057146; PMID:2136251

A; Accession: S12143

A; Accession: S12143

A; Residues: 1-300 cMBS.

A; Residues: 1-300 cMBS.

A; Cross-references: EMBL:X54708; NID:91612; PIDN:CAA38515.1; PID:91613

B; Colburn, P; Crabb, J.W.; Buonassisi, V.

Cell. Physiol. 148, 320-326, 1991

A; Title: Enhanced inhibition of tissue factor by the extended form of an endothelial A; Reference number: A61373; MUID:9149227; PMID:1880157
              A; Molecule type: protein
A; Mosledues: 25.33, 7x, 55-46 <COL>
A; Residues: 25.33, 7x, 55-46 <COL>
C; Superfamily: tissue factor pathway inhibitor; animal Kunitz-type proteinase inhibit C; Keywords: anticoagulant; glycoprotein
F; 50-100/Domain: animal Kunitz-type proteinase inhibitor homology <BP1>
F; 212-1171/Domain: animal Kunitz-type proteinase inhibitor homology <BP2>
F; 213-263/Domain: animal Kunitz-type proteinase inhibitor homology <BP3>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ó
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        61 GNONRFESLEECKKMCTRDNANRIIKTTLQQEKPDFCFLEEDPGICRGYITRYFYNQQTK 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 DSEEDEEHTIITDTELPPLKLMHSPCAFKADDGPCRAIMKRFFFNIFTRQCEEFIYGGCE 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     26 AEEDEEFTNITDIKPPLOKPTHSFCAMKVDDGPCRAYIKRFFFNILAHOCEEFIYGGCEG 85
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  29 DSEEDEEYTIITDTELPPLKLMHSFCAFKPDDGPCKAIMKRFFFNIFTRQCEEFIYGGCG 88
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEEDEEHTIITDTELPPLKLMHSFCAFKADDGPCRAIMKRFFFNIFTROCEEFIYGGCEG 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 304;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             lipoprotein-associated coagulation inhibitor precursor - rabbit
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             6.8e-71;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               121 QCERFKYGGCLGNMNNFETLEECKNICEDGPNGFQVDNYGT 161
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               72.2%; Score 653; DB 2; 72.5%; Pred. No. 9.3e-54;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Pred. No. 6.867; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               13; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 836;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 92.4%;
Best Local Similarity 91.3%;
Matches 147; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 72.2
Best Local Similarity 72.5
Matches 116; Conservative
1-304 <KAM>
```

fa

```
tissue factor pathway inhibitor - rabbit
C;Species: Oryctolagus cuniculus (domestic rabbit)
C;Date: Olyctolagus cuniculus (domestic rabbit)
C;Date: Olyctolagus cuniculus (domestic rabbit)
C;Accession: 85332
R;Girard, T.J.; Gailani, D.; Broze Jr., G.J.
Biochem J. 303, 923-928, 1994
A;Title: Complementary DNA sequencing of canine tissue factor pathway inhibitor revea A;Reference number: S53325; MUID:95071310; PMID:7980463
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Nalternate names: placental protein 5 (PP5)
C;Species: Homo sapiens (man)
C;Species: Homo sapiens (man)
C;Date: 31-May-1996 #sequence_revision 31-May-1996 #text_change 16-Jul-1999
C;Accession: A54951; I55185; A34029; C34029; B34029
R;Sprecher, C.A.; Kislel, W.; Mathewes, S.; Foster, D.C.
R;Sprecher, C.A.; Kislel, W.; Mathewes, S.; Foster, D.C.
A;Jitle: Molecular cloning, expression, and partial characterization of a second huma A;Reference number: A54951; MUID:94211862; PMID:8159751
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          4;
                                                                                                                                                                                         ö
F;134/Inhibitory site: Arg (coagulation factor X) #status predicted F;144,251,261/Binding site: carbohydrate (Asn) (covalent) #status predicted F;232/Inhibitory site: Lys (unidentified proteinase) #status predicted
                                                                                                                                                                                                                                                                                                                                                                            NRFESLEECKKMCTRDNANRIIKTTLQQEKPDFCFLEEDPGICRGYITRYFYNQQTKQCE 123
                                                                                                                                                                                                                                                                                                                                                                                                                91 NRFDTLEECRKTCIPGYKKTTIKTTSGAEKPDFCFLEEDPGICRGFWTRYFYNNQSKQCE 150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             63 ONRFESLEECKKMCTRDNANRIIKT-TLQQ--EKPDFCFLEEDPGICRGYITRYFYNQQT 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                       4 EDEEHTIITDTELPPLKLMHSFCAFKADDGPCRAIMKRFFFNIFTRQCEEFIYGGCEGNQ 63
                                                                                                                                                                                                                                                                                        3 EEDEEHTIITDTELPPLKLMHSFCAFKADDGPCRAIMKRFFFNIFTRQCEEFIYGGCGGN 62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A Status: prolliminary
A; Molecule type: mRNA
A; Molecule type: mRNA
A; Molecule type: mRNA
A; Residues: 1-396 <GIR>
C; Superfamily: animal Kunitz-type proteinase inhibitor homology
C; Keywords: serine proteinase inhibitor
F; 53-103/Domain: animal Kunitz-type proteinase inhibitor homology <BP1>
F; 125-175/Domain: animal Kunitz-type proteinase inhibitor homology <BP2>
F; 309-359/Domain: animal Kunitz-type proteinase inhibitor homology <BP3>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ;
6
                                                                                                                                                                                         .
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 396;
                                                                                                                                                                                      31; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          21; Indels
                                                                                                                        Score 594; DB 1;
Pred. No. 3.1e-48;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; Score 550; DB 2;
; Pred. No. 5.5e-44;
24; Mismatches 21,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         124 RFKYGGCLGNMNNFETLEECKNICEDGPNGFQVDNYGT 161
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             tissue factor pathway inhibitor-2 precursor - human
                                                                                                 65.6%; Scor.
63.8%; Pred. No. 5...
7... 26; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          120 KQCERFKYGGCLGNMNNFETLEECKNICE 148
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Status: translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-235 <RES>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      60.8%;
65.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       98; Conservative
                                                                                                                                                                                         Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity
                                                                                                                                                            Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Accession: S53325
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Accession: A54951
                                                                                                                                                                                         Matches 101;
                                                                                                                               Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Matches
                                                                                                                                                                                                                                                                                                                                                                            64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 7
A54951
                                                                                                                                                                                                                                                       δŽ
                                                                                                                                                                                                                                                                                                               g
                                                                                                                                                                                                                                                                                                                                                                            à
                                                                                                                                                                                                                                                                                                                                                                                                                                       g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ă
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            qq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               d
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        qq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ŏ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      F.1-28/Domain: signal sequence #status predicted <515.0
F.29-302/Product: tissue factor pathway inhibitor #status predicted <MAT>
F.52-103/Domain: animal Kunitz-type proteinase inhibitor homology <BPD>
F.522-272/Domain: animal Kunitz-type proteinase inhibitor homology <BPD>
F.588-291/Predion: animal Kunitz-type proteinase inhibitor homology <BPD>
F.588-291/Predion: heparin binding #status predicted
F.538-103.62-86.78-99,124-174,133-157,149-170,222-272,231-255,247-268/Disulfide bonds: #$
F.637Inhibitory site: Lys (coagulation factor VII/tissue factor complex) #status predict
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            tissue factor pathway inhibitor precursor - rat
N;Alternate names: extrinsic pathway inhibitor; lipoprotein-associated coagulation inhib
C;Species: Rattus norvegicus (Norway rat)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A; Experimental source: liver C; Comment: This serime proteinase inhibitor regulates clotting by factor Xa-dependent in C; Comment: This serime proteinase inhibitor C; Comment: The first Kunitz-type domain binds the factor VIIa/tissue factor complex; the C; Superfamily: tissue factor pathway inhibitor; animal Kunitz-type proteinase inhibitor C; Keywords: anticoagulant; blood coagulation; duplication; glycoprotein; heparin binding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  C;Superfamily: tissue factor pathway inhibitor; animal Kunitz-type proteinase inhibitor F;49-9y-Domain: animal Kunitz-type proteinase inhibitor homology <BPII>F;120-170/Domain: animal Kunitz-type proteinase inhibitor homology <BPI>F;212-262/Domain: animal Kunitz-type proteinase inhibitor homology <BPI>F;212-262/Domain: animal Kunitz-type proteinase inhibitor homology <BPI>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  C; Accession: UX0213
R; Enjyoji, K.; Emi, M.; Mutai, T.; Kato, H.
J. Biochem. 111, 681-687, 1992
A; Title: cDNA cloning and expression of rat tissue factor pathway inhibitor (TFPI).
A; Reference number: UX0213; MUID:92348361; PMID:1639767
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ö
                                                                                                                                                                                                                                                                       C; Species: Orytchagus cuniculus (domestic rabbit)
C; Species: Orytchagus cuniculus (domestic rabbit)
C; Date: 04-Sep-1997 #sequence_revision 04-Sep-1997 #text_change 13-Aug-1999
C; Accession: 146937
R; Belaaouaj, A.; Kuppuswamy, M.N.; Birktoft, J.J.; Bajaj, S.P.
Thromb. Res. 69, 547-553, 1993
A; Title: Revised cDNA sequence of rabbit tissue factor pathway inhibitor.
A; Reference number: 146937; MUID:93276427; PMID:8503123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       C; Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 16-Jun-2000
                             86 NENRFESLEECKEKCARDYPKMTTKLTFQKGKPDFCFLEEDPGICRGYITRYFYNQSKQ 145
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NRFESLEECKKMCTRDNANRIIKTTLQQEKPDFCFLEEDPGICRGYITRYFYNQQTKQCE 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A; Cross-references: DDBJ:D10926; NID:g220916; PIDN:BAA01724.1; PID:g220917
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        4 EDEEHTIITDTELPPLKLMHSFCAFKADDGPCRAIMKRFFFNIFTRQCEEFIYGGCEGNQ 63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Residues: 11.299 <BEL>
A;Cross-references: GB:S61902; NID:9386015; PIDN:AAB26836.1; PID:9386016
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                .;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           71.3%; Score 645; DB 2; Length 299; 72.2%; Pred. No. 5.2e-53;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels
                                                                                                                           146 CERFKYGGCLGNLNNFESLEECKNTCENPTSDFOVDDHRT 185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         30;
                                                                                           CERFKYGGCLGNMNNFETLEECKNICEDGPNGFQVDNYGT 161
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RFKYGGCLGNMNNFETLEECKNICEDGPNGFQVDNYGT 161
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Status: preliminary; translated from GB/EMBL/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         14; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Similarity 72.2%;
14; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A; Molecule type: mRNA
A; Residues: 1-302 <ENJ>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A; Molecule type: mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Accession: JX0213
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Matches 114;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      147
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT 5
                                                                                                                                                                                                                                                    RESULT 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           q
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             q
                             g
                                                                                           δ
                                                                                                                                                     qq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ŏ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           δŏ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Сp
```

A; Map position: 5

Length 1558;

```
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ----TRDNANR----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A; Reference number: 220145
A; Accession: T26063
                                                                                                                            Similarity
                                                                                                                                                                                                                                                                                                                                                            ----TRDNANR-
                                                                                                                                                           52;
                                                                                         Query Match
Best Local S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         C; Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 10
T26063
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1383
                                                                                                                                                           Matches
                                                                                                                                                                                                                                                                                                                                                            11
                                                                                                                                                                                                                                                                                       g
                                                                                                                                                                                                                                                                                                                                                            δλ
                                                                                                                                                                                                                                                                                                                                                                                                                          g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           δy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              δλ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         qq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          δλ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ŏ
A;Cross-references: GB:L27624; NID:g441149; PIDN:AAA20094.1; PID:g441150
A;Experimental source: placenta
R;Miyaqi, Y.; Koshikwaz, N.; Yasamitsu, H.; Miyaqi, E.; Hitahara, F.; Aoki, I.; Misugi,
J. Biocham. 116, 939-942, 1994
A;Title: cDMA cloning and mRNA expression of a serine proteinase inhibitor secreted by
A;Reference number: 155185; MID:95204397; PMID:7896752
A;Resion: 155186
A;Resion: RNA
A;Residues: 1.235 <RE2>
A;Residues: 1.235 <RE2>
A;Residues: 1.235 <RE2>
A;Residues: 1.236 <AREA>
A;Residues: 1.34029
A;Roces-references: GE:192992; NID:9480606; PIDN:BAA06272.1; PID:9484051
A;Residues: 1.34029
A;Roces-reference number: A34029
A;Residues: A34029
A;Residue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           protein C37C3.6a [imported] - Caenorhabditis elegans
C;Species: Caenor C89114
R;anonymous, The C. elegans Sequencing Consortium.
Soience 282, 2012-2018, 1998
A;Title: Genome sequence of the nematode C. elegans: a platform for investigating biolog A;Reference number: A/7000; MUID:99069613; PMID:9851916
A;Note: see websites genome.wustl.edu/gsc/C_elegans/ and www_sanger.ac.uk/Projects/C_ele A;Note: published errata appeared in Science 283, 35, 1999; Science 283, 2103, 1999; and A;Status: preliminary
A;Status: preliminary
A;Status: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Residues: 1-1558 <STO>
A;Cross-references: GB:Chr_V; PIDN:AAC25867.1; PID:g3294501; GSPDB:GN00023; CESP:C37C3.6
C;Genetics:
A;Gene: C3473.6a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                96 CRLQVSVDDQCEGSTEKYFFNLSSMTCEKFFSGGCHRNRIENRFPDEATCMGFCAPKKIP 155
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         94
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  26 CAFKADDGPCRAIMKRFFFNIFTRQCEEFIYGGCEGNQNRFESLEECKKMCTR-DNANRI 84
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     51;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       95 DFCFLEEDPGICRGYITRYFYNQQTKQCERFKYGGCLGNMNNFETLEECKNIC 147
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               30.3%; Score 274.5; DB 2; Length 235; 28.9%; Pred. No. 2e-18; Live 29; Mismatches 43; Indels 51
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  85 IK-----TTLOOEK-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Best Local Similarity 28.9
Matches 50; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                q
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  δy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Pp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            g
```

```
A;Nap position: 5
A;Introns: 32/3; 104/2; 156/2; 207/1; 459/2; 536/3; 577/2; 1105/3; 1367/1; 1438/1; 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Cipecies: Caenorhabditis elegans
Cipecies: Caenorhabditis elegans
Cipecies: Caenorhabditis elegans
Cipecies: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 01-Dec-2000
CiAccession: 734395, 734394
Riceisel, C.: Bradshaw, H.
Submitted to the EMBL Data Library, July 1996
A; Description: The sequence of C. elegans cosmid C37C3.
A; Reference number: 221518
A; Accession: T34395
A; Reference number: 221518
A; Accession: T34395
A; Residues: 1-2167 <GEI>A; CESP:C37C3.6b
A; Residues: L-2167 <GEI>A; CESP:C37C3.6b
A; Residues: Preliminary; translated from GB/EMBL/DDBJ
A; Accession: T34394
A; Status: preliminary; translated from GB/EMBL/DDBJ
A; Accession: T34394
A; Status: preliminary; translated from GB/EMBL/DDBJ
A; Accession: T34394
A; Status: preliminary; translated from GB/EMBL/DDBJ
A; Accession: T34594
A; Status: Preliminary; translated from GB/EMBL/DDBJ
A; Accession: T34504
A; Residues: 1-1555, SRF' <GE2>
A; Cross-references: EMBL:064857; PIDN:AAC25867.1; GSPDB:GN00023; CESP:C37C3.6a
A; Residues: 1-1555, SRF' <GE2>
A; Cross-references: EMBL:064857; PIDN:AAC25867.1; GSPDB:GN00023; CESP:C37C3.6a
                                                                                                                 3,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ä
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 C; Species: Caenorhabditis elegans
C; Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999
C; Accession: T26063
K; Cummings, P.
Submitted to the EMBL Data Library, March 1997
                                                                                                                                                                                                                                                                                                                                                                                                                                         1323 FVHGAQPSAARQEQAQPAAQPAQPAQPSNIVSPPQQSASPVVVPSNSKQRDACHLNVDQG 1382
                                                                                                                                                                                                                                                                         1263 PRQSMEDICRSRQDAGPCETYSDQWFYNAFSQECETFTYGGCGGNLNRFRSKDECEQRCF 1322
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1263 PRQSMEDICRSRQDAGPCETYSDQWFYNAFSQECETFTYGGCGGULNRFRSKDECEQRCF 1322
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1323 FVHGAQPSAARQEQAQPAAQPAQPAQPSNIVSPPQQSASPVVVPSNSKQRDACHLNVDQG 1382
                                                                                                                                                                                                                                                                                                                                                                 -----IIKTTLQQEKP-----DFCFLEEDPG 104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -----DFCFLEEDPG 104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          18 PLKLMHSFCAFKADDGPCRAIMKRFFFNIFTRQCEFFIYGGCEGNQNRFESLEECKKMC-
                                                                                                                                                                                                 18 PLKLMHSFCAFKADDGPCRAIMKRFFFNIFTRQCEFFIYGGCEGNQNRFESLEECKKMC-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          33;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DB 2; Length 2167;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels
                                                                                                                     Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       105 ICRGYITRYFYNQQTKQCERFKYGGCLGNMNNFETLEECKNIC 147
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             105 ICRGYITRYFYNQQTKQCERFKYGGCLGNMNNFETLEECKNIC 147
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 29.4%; Score 266.5; DB 2; Best Local Similarity 31.9%; Pred. No. 1.1e-16; Matches 52; Conservative 23; Mismatches 55;
hypothetical protein C37C3.6b - Caenorhabditis elegans
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   hypothetical protein W01F3.3 - Caenorhabditis elegans
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A; Gene: CESP: C37C3.6b; CESP: C37C3.6a
```

ŝ

Gaps

```
C;Accession: E88550
R;anonymous, The C. elegans Sequencing Consortium.
Science 282, 2012-2018, 1998
A;Title: Genome sequence of the nematode C. elegans: a platform for investigating bio A;Title: Genome sequence of the nematode C. elegans: a platform for investigating bio A;Title: see websites genome.wustl.edu/gsc/C_elegans/ and www_sanger.ac.uk/Projects/C_A;Note: published errata appeared in Science 283, 35, 1999; Science 283, 2103, 1999; A;Accession: E88550
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Cross-references: GB:chr_III; PIDN:CAA79569.1; PID:93881446; GSPDB:GN00021; CESP:ZC A;Note: similar to Serine protease inhibitor, Kunitz type
                                                                                                       A; Cross-references: EMBL: Z75545; PIDN: CAA99886.1; GSPDB: GN00019; CESP: K10D3.4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           C;Species: Caenorhabditis elegans
C;Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 10-May-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    hypothetical protein 2C84.1 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C:Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 29-Aug-1997
C;Accession: S28291
                                                                                                                                                                                                                                                                                                                                                                                                                                                   ------CFLEEDPGI-C- 106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    490 EPKCIQGQAYKDMFGNFVTCSNGMGCPANYECYFDGSQWGCCPTKAFTCSLNTDSGIQCG 549
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 471 IQGTALIDSNGNFIICGGSSAASTICPAN--HYCYYDGTTYGCCPTQAYTCSLSYKSGAS 528
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       432 TICAOPLRIGDCTENVKRYWYNARTROCOMFEYTGCOGNDNNFDSIMDCONFC--KNAIP 489
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   24 SFCAFKADDGPCRAIMKRFFFNIFTRQCEFFIYGGCEGNQNRFESLEECKKMCTRDNANR 83
                                                                                                                                                                                                                                                                                                                                                                   44;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       106 CRGYITRYFYNQQTKQCERFKYGGCLGNMNNFETLEECKNIC--EDGPNGFQV 156
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 1416;
                                                                                                                                                                                                                                                                                                            Length 922;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          107 RGYITRYFYNQQTKQCERFKYGGCLGNMNNFETLEECKNICEDG--PNG 153
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                54; Indels
                                                                                                                                                                                                                                                                                                                                                                53; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                 26 CAFKADDGPCRAIMKRFFFNIFTRQCEEFIYGGCEGNQNRFESLEECKKMC
                                                                                                                                                                                                                      A,Map position: 1
A;Introns: 60/1; 228/1; 278/1; 355/1; 743/1; 802/1; 885/2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      26.7%; Score 241.5; DB 2;
33.1%; Pred. No. 1.6e-14;
Live 18; Mismatches 54;
                                                                                                                                                                                                                                                                                                       27.0%; Score 244; DB 2; 30.1%; Pred. No. 5.9e-15; tive 24; Mismatches 53;
A;Accession: T23573
A;Status: preliminary: translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-922 <WIL>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ----TRDNANRII-----KTTLQQEKPDFCFLE---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  protein ZC84.1 [imported] - Caenorhabditis elegans
                                                                                                                                   A; Experimental source: clone K10D3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Best Local Similarity 33.1%
Matches 56; Conservative
                                                                                                                                                                                                                                                                                                                                                                Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             84 IIKTTLQQEKPDF---
                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A; Molecule type: DNA A; Residues: 1-1416 <STO>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A; Status: preliminary
                                                                                                                                                                                             A; Gene: CESP:K10D3.4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A; Map position: 3
                                                                                                                                                                                                                                                                                                                                                             52;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A; Gene: ZC84.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
                                                                                                                                                                      C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     δλ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        q
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Map position: 5
A;Introns: 31/1; 98/1; 162/1; 199/1; 244/1; 279/1; 323/1; 354/2; 391/1; 408/1; 458/1; 4β
                                                                                              A; Experimental source: clone W01F3
C; Genetics:
A; Genetics:
A; Genetics:
A; Genetics:
A; Map position: 5
A; Introns: 33/1; 56/1; 100/1; 142/3; 271/3; 451/1; 525/3; 774/1; 1093/1; 1178/1; 1221/1;
                                                                                                                                                                                                                                                                                                                                   4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-838 <MIL>
A;Coss-references: EMBL:273971; PIDN:CAA98251.1; GSPDB:GN00023; CESP:C50H2.3a
A;Experimental source: clone C50H2
                    A;Molecule type: DNA
A;Residues: 1-2225 <WIL>
A;Cross-references: EMBL:Z92815; PIDN:CAB07294.1; GSPDB:GN00023; CESP:W01F3.3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               hypothetical protein C50H2.3a - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 15-Oct_1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         hypothetical protein K10D3.4 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                       727 DEBEBEBEBYVEEEQEDGKEEPPLHVQPPVSQQNTVLLGGIEDTTTDSVNRCLHPRDSGNC 786
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LEECKKMCTRDNANRIIKTTLQQEKPDFCFLEEDPGIC---RGYITRYFYNQQTKQCERF 125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           79 KQQCVKQCKYKMFNPV-----AVPDLCLLDADQGHCGDERNGHWWYFFNQESGECEKF 131
                                                                                                                                                                                                                                                                                                                                                                                 1 DSEEDEEHTIITDTE-----LPPLKLMHSF-------CAFKADDGPC 35
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              36 RAIMKRFFFNIFTRQCEEFIYGGCEGNQNRFESLEECKKMCTRDNANRIIKTTLQQEKPD 95
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             11 ITDTELPP--LKLMHSFCAFKADDGPCRAIMKRFFFNIFTRQCEEFIYGGCEGNQNRFES 68
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   96 F---CFLEEDPGICRGYITRYFYNQQTKQCERFKYGGCLGNMNNFETLEECKNIC 147
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 27.8%; Score 252; DB 2; Length 838; Best Local Similarity 35.9%; Pred. No. 9.6e-16; Matches 51; Conservative 23; Mismatches 56; Indels 12;
                                                                                                                                                                                                                                                                                                                                35;
                                                                                                                                                                                                                                                                          Length 2225;
                                                                                                                                                                                                                                                                                                                                Indels
                                                                                                                                                                                                                                                                       DB 2;
                                                                                                                                                                                                                                                                          Score 257.5; DB 2 Pred. No. 7.9e-16;
A;Status: preliminary; translated from GB/EMBL/DDBJ
                                                                                                                                                                                                                                                                                                                             23; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         R;McMurray, A. submitted to the EMBL Data Library, June 1996 A;Reference number: 219226 A;Accession: T20125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        submitted to the EMBL Data Library, June 1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    126 KYGGCLGNMNNFETLEECKNIC 147
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 132 FYYGCGGNDNKFYSLHMCRKVC 153
                                                                                                                                                                                                                                                                          28.5%;
30.9%;
                                                                                                                                                                                                                                                                                                                             54; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Reference number: Z19762
                                                                                                                                                                                                                                                                                                    Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A; Gene: CESP:C50H2.3a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  C; Accession: T20125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               C; Accession: T23573
R; McMurray, A.
                                                                                                                                                                                                                                                                          Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                C;Genetics:
                                                                                                                                                                                                                                                                                                                           Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT 11
                                                                                                                                                                                                                                                                                                                                                                                                                                       Dp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ŏ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           q
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       δy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                δ
```

ŝ

```
d
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              hypothetical protein F30H5.3 - Caenorhabditis elegans
C; Species: Caenorhabditis elegans
C; Species: Caenorhabditis elegans
C; Species: Caenorhabditis elegans
C; Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 20-Sep-1999
C; Accession: T16210
R; Pauley, A.; Stellyes, L.
Submitted to the EMBL Data Library, June 1995
A; Rederence number: 218478
A; Reference number: 218478
A; Reference number: 218478
A; Reference number: Drail array; translated from GB/EMBL/DDBJ
A; Reaidues: 1-1599 < RAUS
A; Residues: 1-1599 < RAUS
A; Residues: 1-1599 < RAUS
A; Cross-references: EMBL:U29096; NID:g861390; PID:g861393; PIDN:AAA68408.1; CESP:F30H5.3
A; Cross-references: EMBL:U29096; NID:g861390; NID:g8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A.Introns: 14/1; 32/3; 57/1; 192/3; 277/1; 398/1; 439/1; 474/1; 497/1; 813/1; 1135/1; 12493/1; 2555/1; 2720/1; 2739/3; 2819/1
C; Superfamily: animal Kunitz-type proteinase inhibitor homology (BPII) P; 220-274/Domain: animal Kunitz-type proteinase inhibitor homology (BPII) P; 343-395/Domain: animal Kunitz-type proteinase inhibitor homology (BPII) P; 342-492/Domain: animal Kunitz-type proteinase inhibitor homology (BPII) P; 546-598/Domain: animal Kunitz-type proteinase inhibitor homology (BPII) P; 1662-1716/Domain: animal Kunitz-type proteinase inhibitor homology (BPII) P; 1861-1895/Domain: animal Kunitz-type proteinase inhibitor homology (BPII) P; 1861-1895/Domain: animal Kunitz-type proteinase inhibitor homology (BPII) P; 1862-1706/Domain: animal Kunitz-type proteinase inhibitor homology (BPII) P; 1862-1706/Domain: animal Kunitz-type proteinase inhibitor homology (BPII) P; 1862-2004/Domain: animal Kunitz-type proteinase inhibitor homology (BPII) P; 1862-2004/Domain: animal Kunitz-type proteinase inhibitor homology (BPII) P; 2097-2152/Domain: animal Kunitz-type proteinase inhibitor homology (BPII) P; 2097-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            615 NIIPEPQCPQGDAYKDYQGNYYVCSNSGAGNSCPVNYECYFDGYVWGCCPTKAYTCTLSP 674
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   75 -------QEKPDFCFLEE 101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ----CFLEEDPGI-C- 106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     498 EPKCIQGQAYKDMFGNFVTCSNGMGCPANYECYFDGSQWGCCPTKAFTCSLNTDSGIQCG 557
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        18 PLKLMHSFCAFKADDGPCRAIMKRFFFNIFTRQCEFFIYGGCEGNQNRFESLEECKK--- 74
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SFCAFKADDGPCRAIMKRFFFNIFTRQCEEFIYGGCEGNQNRFESLEECKKMCTRDNANR 83
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 103 DPGI-C-RGYITRYFYNQQTKQCERFKYGGCLGNMNNFETLEECKNICEDG--PNG 153
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      26.6%; Score 240.5; DB 2; Length 1599; 31.2%; Pred. No. 2.2e-14; tive 21; Mismatches 49; Indels 51;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               26.7%; Score 241.5; DB 2; Length 2844; 33.1%; Pred. No. 3.2e-14; Live 18; Mismatches 54; Indels 41;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 107 RGYITRYFYNQQTKQCERFKYGGCLGNMNNFETLEECKNICEDG--PNG 153
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               84 IIKTTLQQEKPDF-----
R;Thomas, K. submitted to the EMBL Data Library, December 1992 submitted to the EMBL 528285 A;Reference number: $28291 A;Accession: $28291
                                                                                                                                                                                                                                                                                                                                                                                                            A; Cross-references: EMBL: 219157
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 31.2'
Matches 55; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Local Similarity
nes 56; Conserva
                                                                                                                                                                                                                                                                                                  A; Molecule type: DNA
A; Residues: 1-2844 <THO>
                                                                                                                                                                                                                                           A;Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   q
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         õ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                q
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            δŏ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          δy
```

```
2, 2002, 10:04:56
                        December
```

Search completed: Decemb Job time: 31.8358 secs

```
GenCore version 5.1.3
Copyright (c) 1993 - 2002 Compugen Ltd.
```

OM protein - protein search, using sw model

December 2, 2002, 10:00:50; Search time 15.2189 Seconds (without alignments) 168.461 Million cell updates/sec Run on:

US-09-741-106-19 905 Title: Perfect score:

1 DSEEDEEHTIITDTELPPLK......ECKNICEDGPNGFQVDNYGT 161 Scoring table: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5

102317 seqs, 15924203 residues Searched:

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Published\_Applications\_AA:\* Database

(cgn2\_6/ptodata/1/pubpaa/US08\_NEW\_PUB.pep:\*
(cgn2\_6/ptodata/1/pubpaa/PCT\_NEW\_PUB.pep:\*
(cgn2\_6/ptodata/1/pubpaa/US06\_NEW\_PUB.pep:\*
(cgn2\_6/ptodata/1/pubpaa/US06\_NEW\_PUB.pep:\*
(cgn2\_6/ptodata/1/pubpaa/US07\_NEW\_PUB.pep:\*
(cgn2\_6/ptodata/1/pubpaa/US07\_NEW\_PUB.pep:\*
(cgn2\_6/ptodata/1/pubpaa/US08\_PUBCOMB.pep:\*
(cgn2\_6/ptodata/1/pubpaa/US08\_PUBCOMB.pep:\*
(cgn2\_6/ptodata/1/pubpaa/US09\_PUBCOMB.pep:\*
(cgn2\_6/ptodata/1/pubpaa/US09\_PUBCOMB.pep:\*
(cgn2\_6/ptodata/1/pubpaa/US09\_PUBCOMB.pep:\*
(cgn2\_6/ptodata/1/pubpaa/US09\_PUBCOMB.pep:\*
(cgn2\_6/ptodata/1/pubpaa/US09\_PUBCOMB.pep:\* /cgn2\_6/ptodata/1/pubpaa/US10\_PUBCOMB.pep:\* /cgn2\_6/ptodata/1/pubpaa/US60\_NEW\_PUB.pep:\* /cgn2\_6/ptodata/1/pubpaa/US60\_PUBCOMB.pep:\* 110: 111: 143:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

					COLUMNIC	
		æ				
Result		Query				
No.	Score	Match	Match Length DB	DB	QI	Description
-	897	99.1	276	6	US-10-086-176A-5	Sequence 5, Appli
7	897	99.1	276	10	US-09-766-778-1	Sequence 1, Appli
m	327	36.1	58	10	US-09-957-607-47	Sequence 47, Appl
4	297	32.8	58	10	US-09-957-607-48	Sequence 48, Appl
S	288	31.8	51	10	US-09-827-948-5	Sequence 5, Appli
9	283	31.3	51	10	US-09-827-948-4	Sequence 4, Appli
7	274.5	30.3	213	6	US-10-086-176A-6	
80	274.5	30.3	213	10	US-09-766-778-2	Sequence 2, Appli
σ	274.5	30.3	235	σ	US-09-736-457-332	Sequence 332, App
10	274.5	30.3	235	6	US-09-902-941-332	Sequence 332, App
11	274.5	30.3	235	10	US-09-904-621-2	Sequence 2, Appli
12	232	25.6	252	10	US-09-827-948-2	
13	232	25.6	289	10	US-09-925-301-1266	Sequence 1266, Ap
14	212.5	23.5	513	10	US-09-765-449-18	Sequence 18, Appl
15	204.5	22.6	529	10	US-09-742-201-2	Sequence 2, Appli
16	199.5	22.0	366	10	US-09-925-301-1175	Sequence 1175, Ap
17	199	22.0	576	10	US-09-794-589-2	Sequence 2, Appli
18	193	21.3	51	10	US-09-827-948-28	Sequence 28, Appl
19	174.5	19.3	548	10	US-09-819-136-2	Sequence 2, Appli

Sequence 55, Appl Sequence 55, Appl Sequence 55, Appl Sequence 5, Appl Sequence 5, Appl Sequence 5, Appl Sequence 59, Appl Sequence 51, Appl Sequence 51, Appl Sequence 51, Appl Sequence 57, Ap	sednence 4, Appli
US-09-794-927-55 US-09-794-413-55 US-09-794-743-55 US-09-904-987-2 US-09-904-987-2 US-09-149-718-6 US-09-149-718-6 US-09-149-718-6 US-09-794-927-59 US-09-794-743-59 US-09-794-748-59 US-09-794-748-59 US-09-794-748-59 US-09-794-788-46 US-09-791-988-46 US-09-791-988-46 US-09-781-988-46 US-09-781-988-46 US-09-781-988-47 US-09-781-988-47 US-09-781-988-47 US-09-781-988-47 US-09-781-988-47 US-09-781-988-47 US-09-794-743-57 US-09-794-743-57 US-09-794-927-57 US-09-794-927-57 US-09-794-925-57 US-09-794-925-57	US-U9-149-/18-4
	7
777000777000777000777000777700077777777	TC/
188.55 188.55 188.55 188.55 188.55 177.77 177.77 177.77 177.77 177.77 177.77 177.77 177.77 177.77 177.77	7.7
100 100 100 100 100 100 100 100 100 100	154.5
01000000000000000000000000000000000000	C #

# ALIGNMENTS

US-10-086-176A-5

```
APPLICANT: Papathanassiu, Adonia E.
APPLICANT: Papathanassiu, Adonia E.
APPLICANT: Green, Shawn J.
TILE OF INVENTION: Compositions and Methods for Inhibiting Cellular Proliferation
TITLE OF INVENTION: TFPI Fragments
FILE REFERENCE: 05213-0296 43170-266780
CURRENT APPLICATION NUMBER: US/10/086,176A
CURRENT FILING DATE: 2002-02-28
PRIOR APPLICATION NUMBER: US 09/766,778
PRIOR APPLICATION NUMBER: US 09/727,955
PRIOR PILING DATE: 1999-01-11
PRIOR FILING DATE: 1999-01-11
PRIOR FILING DATE: 1999-02-06
PRIOR FILING DATE: 1999-03-06
PRIOR FILING DATE: 1999-03-06
PRIOR FILING DATE: 1999-03-06
NUMBER OF SEQ ID NOS: 6
SOFTWARE: PatentIn Version 3.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     61 GNQNRFESLEECKKMCTRDNANRIIKTTLQQEKPDFCFLEEDPGICRGYITRYFYNQQTK 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             61 GNQNRFESLEECKKMCTRDNANRIIKTTLQQEKPDFCFLEEDPGICRGYITRYFYNNQTK 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          99.1%; Score 897; DB 9; Length 276; 98.8%; Pred. No. 1.4e-81; tive 1; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; OTHER INFORMATION: Synthetic peptide US-10-086-176A-5
Sequence 5, Application US/10086176A Patent No. US/20020173465A1 GENERAL INFORMATION: APPLICANT: Hembrough, Todd
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 99.1%
Best Local Similarity 98.8%
Matches 159; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQ ID NO 5
LENGTH: 276
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     q
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          δλ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  q
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     δλ
```

á g

```
NAME/KEY: Active-site
LOCATION: 228..229
QTHER INFORMATION: /note= "Potential site for N-linked
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME/KEY: Active-site
LOCATION: 117..118
OTHER INFORMATION: /note= "Potential site for N-linked
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME/KEY: Active-site
LOCATION: 167..168
OTHER INFORMATION: /note- "Potential site for N-linked
                                                                                                                                                                                                                                         Arritania Creen, Shawn J.

Green, Shawn J.

TITLE OF INVENTION: Compositions and Methods for Inhibiting
Cellular Proliferation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/766,778
FILING DATE: 22-Jan-2001
CLASSIFICATION UNMBER: 09/227,955
FILING DATE: CURRENT COMPATA:
APPLICATION NUMBER: 09/227,955
FILING DATE: AURHOWN>
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LOCATION: 2..3
OTHER INFORMATION: /note= "Site of partial
121 QCERFKYGGCLGNMNNFETLEECKNICEDGPNGFQVDNYGT 161
                       CORRESPONDENCE ADDRESS:
ADDRESSEE: Jones & Askew
STREET: 191 Peachtree Street, 37th Floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME: Greene, Jamle L.
REGISTRATION NUMBER: 32,467
REFERENCE/DOCKET NUMBER: 05213-0290
TELECOMMUNICATION INFORMATION:
TELEPHONE: (404) 818-3700
                                                                                                                                                                                                                             APPLICANT: Papathanassiu, Adonia E
                                                                                                                                                          Sequence 1, Application US/09766778 Patent No. US20010018204A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEFAX: (404) 818-3799
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LENGTH: 276 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME/KEY: Active-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FRAGMENT TYPE: N-terminal ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                STATE: Georgia
COUNTRY: U.S.A.
ZIP: 30303
COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TOPOLOGY: linear MOLECULE TYPE: protein HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              phosphorylation"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            glycosylation"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              glycosylation"
                                                                                                                                                                                                                                                                                                                                                                                                                CITY: Atlanta
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ANTI-SENSE: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FEATURE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FEATURE
                                                                                                             RESULT 2
US-09-766-778-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FEATURE
```

```
ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        61 GNQNRFESLEECKKMCTRDNANRIIKTTLQQEKPDFCFLEEDPGICRGYITRYFYNQQTK 120
                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                        1 DSEEDEEHTIITDTELPPLKLMHSFCAFKADDGPCRAIMKRFFFNIFTRQCEEFIYGGCE 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Maclenan, John M.
APPLICANT: Maclenan, John M.
APPLICANT: Ladner, Robert C.
TITLE OF INVENTION: Engineering Affinity Ligands for Macromolecules
FILE REFERENCE: DYX-00.1 US-1
CURRENT APPLICATION NUMBER: US/09/957,607
CURRENT FILING DATE: 2001-09-19
PRIOR APPLICATION UNMER: 08/821,498
PRIOR APPLICATION NUMBER: 08/821,498
PRIOR APPLICATION NUMBER: 08/81,498
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 48, Application US/09957607
Patent No. US20020076728al
GENERAL INFORMATION:
APPLICANT: Maclennan, John M.
APPLICANT: Ladner, Robert C.
TITLE OF INVENTION: Engineering Affinity Ligands for Macromolecules
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 MHSFCAFKADDGPCKAIMKRFFFNIFTRQCEEFIYGGCEGRONRFESLEECKKMCTRD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  22 MHSFCAFKADDGPCRAIMKRFFFNIFTRQCEEFIYGGCEGNQNRFESLEECKKMCTRD
                                                                                                                                                                                                                                                                                                                                                                              ó;
                                                                                                                                                                                                                                                                                                                                   99.1%; Score 897; DB 10; Length 276; 98.8%; Pred. No. 1.4e-81; Live 1; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                36.1%; Score 327; DB 10; Length 58; 98.3%; Pred. No. 4.8e-26;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    121 QCERFKYGGCLGNMNNFETLEECKNICEDGPNGFQVDNYGT 161
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       OTHER INFORMATION: /label= Kunitz-3 SEQUENCE DESCRIPTION: SEO ID NO: 1:
                                                                                      /label= Kunitz-1
                                                                                                                                                                   /label= Kunitz-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US-09-957-607-47
; Sequence 47, Application US/09957607
; Patent No. US20020076728A1
; GENERAL INFORMATION:
                                                                                                                                                                                                                                LOCATION: 189..239
OTHER INFORMATION:
                                                                                                                                              LOCATION: 97..147
OTHER INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NUMBER OF SEQ ID NOS: 48
SOFTWARE: Patentin version 3.1
SEQ ID NO 47
EBNCTH: 58
                                                                LOCATION: 26..76
OTHER INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRIOR FILING DATE: 1996-03-20
                                        NAME/KEY: Domain
LOCATION: 26..76
                                                                                                                            NAME/KEY: Domain
                                                                                                                                                                                                              Domain
                                                                                                                                                                                                                                                                                                                                                        Best Local Similarity 98.8
Matches 159; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         57; Conservative
glycosylation"
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; ORGANISM: Homo sapiens
US-09-957-607-47
                                                                                                                                                                                                            NAME/KEY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Best Local Similarity
                                                                                                                                                                                         FEATURE:
                                                                                                         FEATURE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 4
US-09-957-607-48
                                                                                                                                                                                                                                                                                          US-09-766-778-1
                                                                                                                                                                                                                                                                                                                                     Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    δy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           qq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ŏ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Dp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Óγ
```

```
Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Ω
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  δλ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           õ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     .
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 22 MHSFCAFKADDGPCRAIMKRFFFNIFTRQCEEFIYGGCEGNQNRFESLEECKKMCTRD 79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            OCHER INFORMATION: X is M.A.C.D.E.F.G.H.I.K.L.N.P.Q.R.S.T.V.W or Y TORMEYKEY MISC_FEATURE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  .;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           97 CFLEEDPGICRGYITRYFYNQQTKQCERFKYGGCLGNMNNFETLEECKNIC 147
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   31.8%; Score 288; DB 10; Length 51; 96.1%; Pred. No. 3e-22; tive 0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 32.8%; Score 297; DB 10; Length 58; Best Local Similarity 89.7%; Pred. No. 4.4e-23; Matches 52; Conservative 1; Mismatches 5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    OTHER INFORMATION: amino acid sequence of LACI/F library NAME/KEY: MISC_FEATURE LOCATION: (13)...(13) OTHER INFORMATION: X is P,H,L, or R NAME/KEY: MISC_FEATURE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LOCATION: (17)...(17)...
OTHER INFORMATION: X is I.A.C.D.F.G.H.L.N.P.R.S.T.V OF Y
NAME/KEY: MISC_FEATURE
LOCATION: (18)...(18)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Stu-An APPLICANT: Rosen, Craig A. APPLICANT: Rosen, Craig A. APPLICANT: Rosen, Craig A. TITLE OF INVENTION: Tissue Factor Pathway Inhibitor-3 FILE REFERENCE: 1488.1290002 CURRENT APPLICATION NUMBER: US/09/827,948 CURRENT FILING DATE: 2001-04-06 PRIOR FILING DATE: 1998-01-27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; LOCATION: (19)..(19)
; OTHER INFORMATION: X is K,A,E,G,L,M,P,Q,R,S,T,V or W
US-09-957-607-48
FILE REFERENCE: DXX-001.1 US-1
CURRENT APPLICATION NUMBER: US/09/957,607
CURRENT FILING DATE: 2001-09-19
PRIOR APPLICATION NUMBER: 08/821,498
PRIOR PILING DATE: 1997-03-21
PRIOR PILING DATE: 1997-03-20
PRIOR PILING DATE: 1996-03-20
NUMBER OF SEQ ID NOS: 48
SOFWARE: PATENTIN VERSION 3.1
LENGTH: 58
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 5, Application US/09827948 Patent No. US20010029034A1
                                                                                                                                                                                                                                                                                                                                                                                                                LOCATION: (16)..(16)
OTHER INFORMATION: X is A OF G
NAME/KEY: MISC_FEATURE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SOFTWARE: PatentIn version 3.0
                                                                                                                                                                                                                                                                ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GENERAL INFORMATION:
APPLICANT: Gentz, Reiner, L.
APPLICANT: Hsu, Tsu-An
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NUMBER OF SEQ ID NOS: 31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Best_Local Similarity
Matches 49; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; ORGANISM: Human
US-09-827-948-5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-09-827-948-5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQ ID NO 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
                                                                                                                                                                                                                                                TYPE: PRT
                                                                                                                                                                                                                                                                                    FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ρp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ŏ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   g
```

```
APPLICANT: Hembrough, Todd
APPLICANT: Papathanassiu, Adonia E.
APPLICANT: Hembrough, Todd
APPLICANT: Papathanassiu, Adonia E.
APPLICANT: Papathanassiu, Adonia E.
TITLE CANT: Green, Shawn J.
TITLE OF INVENTION: Compositions and Methods for Inhibiting Cellular Proliferation
TITLE OF INVENTION: TFPI Fragments
FILE REFERENCE: 05213-0296 43170-266780
CURRENT FILING DATE: 2002-02-28
PRIOR FILING DATE: 2001-01-22
PRIOR APPLICATION NUMBER: US 09/766,778
PRIOR APPLICATION NUMBER: US 08/796,850
PRIOR FILING DATE: 1999-01-11
PRIOR PILING DATE: 1999-01-11
PRIOR FILING DATE: 1999-06-06
PRIOR FILING DATE: 1999-08-06
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ë
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   51; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         14 CLLPLDYGPCRALLLRYYYDRYTQSCRQFLYGGCGGNANNFYTWEACDDACWRIEKVPKV 73
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              26 CAFKADDGPCRAIMKRFFFNIFTRQCEFFIYGGCEGNQNRFESLEECKKMCTR-DNANRI 84
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ---- 94
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              30.3%; Score 274.5; DB 9; Length 213; 28.9%; Pred. No. 3e-20;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  26 CAFKADDGPCRAIMKRFFFNIFTRQCEEFIYGGCEGNQNRFESLEECKKMC 76
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 51;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   43; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1; Indels
                                                                                  APPLICANT: Gentz, Reiner, L.
APPLICANT: Hsu, Tsu-An
APPLICANT: No. An. Craig A.
APPLICANT: No. An. Craig A.
TITLE OF INVENTION: Tissue Factor Pathway Inhibitor-3
FILE REFERENCE: 1488.1290002
CURRENT APPLICATION NUMBER: US/09/827,948
CURRENT APPLICATION NUMBER: US 09/013,896
PRIOR APPLICATION NUMBER: US 09/013,896
PRIOR FILING DATE: 1998-01-27
NUMBER OF SEQ. ID NOS: 31
SOFTWARE: Patentin version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 283; DB 10;
Pred. No. 9.3e-22;
1; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                29; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ----TILQQEK---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; OTHER INFORMATION: Synthetic peptide US-10-086-176A-6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; Sequence 6, Application US/10086176A ; Patent No. US20020173465A1
                ; Sequence 4, Application US/09827948
; Patent No. US20010029034A1
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              31.3%;
96.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SOFTWARE: Patentin version 3.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Best Local Similarity 28.99
Matches 50; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NUMBER OF SEQ ID NOS: 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GENERAL INFORMATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       85 IK-----
                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: PRT
ORGANISM: Human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-10-086-176A-6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            49:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQ ID NO 6
LENGTH: 213
                                                                                                                                                                                                                                                                                                                                                                                                                                                                US-09-827-948-4
JS-09-827-948-4
                                                                                                                                                                                                                                                                                                                                                           SEQ ID NO 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            δλ
```

a ÓΣ g

```
δλ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     74 CRLQVSVDDQCEGSTEKYFFNLSSMTCEKFFSGGCHRNRIENRFPDEATCMGFCAPKKIP 133
74 CRLQVSVDDQCEGSTEKYFFNLSSMTCEKFFSGGCHRNRIENRFPDEATCMGFCAPKKIP 133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     P6 d------ 84
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             26 CAFKADDGPCRAIMKRFFFNIFTRQCEEFIYGGCEGNQNRFESLEECKKMCTR-DNANRI 84
                                                                                                                                                                                                                                                                           APPLICANT: Papthanassiu, Adonia E
Green, Shawn J.
TITLE OF INVENTION: Compositions and Methods for Inhibiting
Cellular Proliferation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           30.3%; Score 274.5; DB 10; Length 213; 28.9%; Pred. No. 3e-20; Live 29; Mismatches 43; Indels 51;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   95 DFCFLEEDPGICRGYITRYFYNQQTKQCERFKYGGCLGNMNNFETLEECKNIC 147
                                                95 DFCFLEEDPGICRGYITRYFYNQQTKQCERFKYGGCLGNMNNFETLEECKNIC 147
                                                                      COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                  CORRESPONDENCE ADDRESS:
ADDRESSEE: Jones & Askew
STREET: 191 Peachtree Street, 37th Floor
CITY: Atlanta
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         85 IK------TTLQQEK-------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME: Greene, Jamie L.
REGISTRATION NUMBER: 32,467
REFERENCE/DOCKET NUMBER: 05213-0290
TELECOMMUNICATION INFORMATION:
TELEPHONE: (404) 818-3700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/766,778
FILLING DATE: 22-Jan-2001
CLASSIFICATION: «Unknown»
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/227,955
FILING DATE: «Unknown»
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ORGANISM: Homo sapiens
SEQUENCE DESCRIPTION: SEQ ID NO: 2:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                            Sequence 2, Application US/09766778 Patent No. US20010018204A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (404) 818-3799
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LENGTH: 213 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          HYPOTHETICAL: NO
ANTI-SENSE: NO
FRAGMENT TYPE: N-terminal
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TOPOLOGY: linear MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STATE: Georgia
COUNTRY: U.S.A.
ZIP: 30303
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  IYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 50; Conservative
                                                                                                                                                                                                                                                                                                                                                                               NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-09-766-778-2
                                                                                                                                                                  RESULT 8
US-09-766-778-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Matches
```

g δ g ò

```
96 CRLQVSVDDQCEGSTEKYFFNLSSMTCEKFFSGGCHRNRIENRFPDEATCMGFCAPKKIP 155
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              26 CAFKADDGPCRAIMKRFFFNIFTRQCEEFIYGGCEGNQNRFESLEECKKMCTR-DNANRI 84
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          36 CLLPLDYGPCRALLLRYYYDRYTQSCRQFLYGGCEGNANNFYTWEACDDACWRIEKVPKV 95
                                                                                                                                                                                                                                                                                                                          TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND TITLE OF INVENTION: DIAGNOSIS OF LUNG CANCER FILE REFERENCE: 210121.478C15
CURRENT APPLICATION NUMBER: US/09/736,457
CURRENT FILING DATE: 2000-12-13
NUMBER OF SEQ ID NOS: 1864
SOFTWARE: FastSEQ for Windows Version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                95 DFCFLEEDPGICRGYITRYFYNQQTKQCERFKYGGCLGNMNNFETLEECKNIC 147
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 235;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER FILE REFERENCE: 210121.478C17
CURRENT APPLICATION UNDBER: US/09/902,941
CURRENT FILING DATE: 2001-07-10
NUMBER OF SEQ ID NOS: 2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    30.3%; Score 274.5; DB 9; 28.9%; Pred. No. 3.3e-20; tive 29; Mismatches 43;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -----TILQQEK-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SOFTWARE: FastSEQ for Windows Version 4.0 SEQ ID NO 332 LENGTH: 235 TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 332, Application US/09902941 Patent No. US20020172952A1
                                       Sequence 332, Application US/09736457 Patent No. US20020168637A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Wang, Tongtong
APPLICANT: Watanabe, Yoshihiro
APPLICANT: Johnson, Jeffrey C.
APPLICANT: Retter, Marc W.
APPLICANT: Mannerakis, Margarita
APPLICANT: Carter, Darrick
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Carter, DALLELSANT: APPLICANT: Fanger, Gary R.
APPLICANT: Vedvick, Thomas S.
APPLICANT: Bangur, Chaitanya S.
TOTTICANT: Monabb, Andria
                                                                                                          Wang, Tongtong
Bangur, Chaitanya S.
Lodes, Michael A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Henderson, Robert A.
                                                                                                                                                                             Fanger, Gary
Vedvick, Tom
Carter, Darrick
Retter, Marc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Best Local Similarity 28.9
Matches 50; Conservative
                                                                                                                                                                                                                                                                     Mannion, Jane
                                                                                                                                                                                                                                                                                          Fan, Liqun
Wang, Aijun
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: PRT ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      85 IK-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GENERAL INFORMATION:
                                                                                          GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-09-902-941-332
RESULT 9
US-09-736-457-332
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-09-736-457-332
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SOFTWARE: Fa
SEQ ID NO 332
LENGTH: 235
                                                                                                                                                                                                  APPLICANT:
APPLICANT:
                                                                                                                                                                                                                                              APPLICANT:
APPLICANT:
                                                                                                          APPLICANT:
                                                                                                                                                        APPLICANT:
                                                                                                                                                                               APPLICANT:
                                                                                                                                                                                                                                                                                          APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
                                                                                                                                                                                                                                                                                                              APPLICANT:
```

٠. ش

3,

```
Dp
                                                                                                                                                                                                                                                                                                                                                                                                                                             qq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     QΩ
                                                                                                                                                                                                                                                                                                                                  ò
                                                                                                                                                                                                                                                                                                                                                                                                         ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         õ
                                                                                               3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ÷
                                                                                                                                                                                                                                        : :: 11
96 CRLQVSVDDQCEGSTEKYFFNLSSMTCEKFFSGGCHRNRIENRFPDEATCMGFCAPKKIP 155
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             96 CRLQVSVDDQCEGSTEKYFFNLSSMTCEKFFSGGCHRNRIENRFPDEATCMGFCAPKKIP 155
                                                                                               51; Gaps
                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      26 CAFKADDGPCRAIMKRFFFNIFTRQCEEFIYGGCEGNQNRFESLEECKKMCTR-DNANRI 84
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                26 CAFKADDGPCRAIMKRFFFNIFTRQCEEFIYGGCEGNQNRFESLEECKKMCTR-DNANRI 84
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Kisiel, Walter
APPLICANT: Kisiel, Walter
TITLE OF INVENITION: NOVEL HUMAN KUNITZ-TYPE INHIBITORS
TITLE OF INVENITION: AND
TITLE OF INVENITION: METHODS RELATING THERETO
FILE REFERENCE: 93-14D3
CURRENT APPLICATION NUMBER: US/09/904,621
CURRENT FILING DATE: 2001-07-13
PRIOR PILIATION NUMBER: EARLIER APPLICATION NUMBER: 09/265,627
PRIOR FILING DATE: EARLIER FILING DATE: 1999-03-09
PRIOR PLILING DATE: EARLIER FILING DATE: 1999-103-09
PRIOR FILING DATE: EARLIER FILING DATE: 1993-11-05
NUMBER OF SEO ID NOS: 15
SOFTWARRE: FASTSEQ for Windows Version 3.0
                                                                                                                                                                                                                                                                                      95 DFCFLEEDPGICRGYITRYFYNQQTKQCERFKYGGCLGNMNNFETLEECKNIC 147
                                                                                                                                                                                                                                                                                                          DB 10; Length 235;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   95 DFCFLEEDPGICRGYITRYFYNQQTKQCERFKYGGCLGNMNNFETLEECKNIC 147
                                                           Length 235;
                                                                                                                                                                                                          85 IK-------TTLQQEK------
                                                                                               Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GENERAL INFORMATION:
APPLICANT: Gentz, Reiner, L.
APPLICANT: Hsu, Tsu-An
APPLICANT: Rosen, Craig A.
APPLICANT: No. Jian
IITLE OF INVENTION: Tissue Factor Pathway Inhibitor-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 30.3%; Score 274.5; DB 10; Best Local Similarity 28.9%; Pred. No. 3.3e-20; Matches 50; Conservative 29; Mismatches 43;
                                                                                               43;
                                                         DB 9;
                                                       30.3%; Score 274.5; DB 9 28.9%; Pred. No. 3.3e-20;
                                                                                             29; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 2, Application US/09904621
Patent No. US200200098560A1
GENERAL INFORMATION:
APPLICANT: Sprecher, Cindy A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 2, Application US/09827948
Patent No. US20010029034A1
                                                                                             50; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; ORGANISM: Homo sapiens US-09-904-621-2
ORGANISM: Homo sapiens
                                                                             Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          85 IK-----
 ; OKGANAL....US-09-902-941-332
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQ ID NO 2
LENGTH: 235
                                                                                                                                                                                                                                                                                                                                                                                                     US-09-904-621-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-09-827-948-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: PRT
                                                         Query Match
                                                                                             Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 12
                                                                                                                                                                     g
                                                                                                                                                                                                                                                g
                                                                                                                                   δλ
                                                                                                                                                                                                              δλ
                                                                                                                                                                                                                                                                                      οy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                δy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    q
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Ω
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Д
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     δy
```

```
:| || | | | | | | | | | | :::|:
52 IHDFCLVSKVVGRCRASMPRWYNVTDGSCQLFVYGGCDGNSNNYLTKEECLKKCATVTE 111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            80 NANRIIKTT-------LQQEKPD------FCFLEEDPGICRGYIIRXFYNQ 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            94 NATGDLATSRNAADSSVPSAPRRQDSEDHSSDMFNYEEYCTANAVTGPCRASFPRWYFDV 153
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        80 NANRIIKTT------LQQEKPD------FCFLEEDPGICRGYITRYFYNQ 117
                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       112 NATGDLATSRNAADSSVPSAPRRQDSEDHSSDMFNYEEYCTANAVTGPCRASFPRWYFDV 171
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    34 IHDFCLVSKVVGRCRASMPRWWYNVTDGSCQLFVYGGCDGNSNNYLTKEECLKKCATVTE 93
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                22 MHSFCAFKADDGPCRAIMKRFFFNIFTRQCEFFIYGGCEGNQNRFESLEECKKMC--TRD 79
                                                                                                                                                                                                                                                                                                                                                                                                                                         22 MHSFCAFKADDGPCRAIMKRFFFNIFTRQCEEFIYGGCEGNQNRFESLEECKKMC--TRD 79
                                                                                                                                                                                                                                                                                                                                                                                       24;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                24;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Rosen et al.
TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
FILE REPERENCE: PAl06
CURRENT APPLICATION NUMBER: US/09/925,301
CURRENT FILING DATE: 2001-08-10
PRIOR APPLICATION NUMBER: CO/124,270
PRIOR APPLICATION NUMBER: 60/124,270
PRIOR FILING DATE: 1999-03-12
NUMBER OF SEQ ID NOS: 1694
SOFTWARE: Patentin Ver: 2.0
SEQ ID NO 1266
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 289;
                                                                                                                                                                                                                                                                                                                                       Length 252;
                                                                                                                                                                                                                                                                                                                                                                                          56; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  56; Indels
                                                                                                                                                                                                                                                                                                                                    ch 25.6%; Score 232; DB 10; I. Similarity 30.7%; Pred. No. 5.5e-16; 46; Conservative 24; Mismatches 56;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ch 25.6%; Score 232; DB 10;
1 Similarity 30.7%; Pred. No. 6.4e-16;
46; Conservative 24; Mismatches 56;
                     CURRENT APPLICATION NUMBER: US/09/827,948
CURRENT FILING DATE: 2001-04-06
PRIOR APPLICATION NUMBER: US 09/013,896
PRIOR FILING DATE: 1998-01-27
NUMBER OF SEQ ID NOS: 31
SOFTWARE: PatentIn version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              118 QTKQCERFKYGGCLGNMNNFETLEECKNIC 147
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              118 QTKQCERFKYGGCLGNMNNFETLEECKNIC 147
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; Sequence 1266, Application US/09925301; Patent No. US20020052308A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT 14
US-09-765-449-18
Sequence 18, Application US/09765449
; Patent No. US20020098537A1
FILE REFERENCE: 1488.1290002
                                                                                                                                                                                                                            TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: PRT
CORGANISM: Homo sapiens
US-09-925-301-1266
                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-09-925-301-1266
                                                                                                                                                                             SEQ ID NO 2
LENGTH: 252
                                                                                                                                                                                                                                                                                    US-09-827-948-2
                                                                                                                                                                                                                                                                                                                                                                                       Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Matches
```

'n

```
δŏ
                                                                                                                                                                                                                                                                                                                                                                                                                                       g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     δy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                q
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              δλ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       qq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 2, Application US/09742201

Sequence 2, Application US/09742201

Sequence 2, Application US/09742201

Sequence 2, Application US/09742201

Sequence 2, Application US/090123091A1

Sequence 2, Application:

APPLICANT: Gurney, Austin L.

APPLICANT: Gurney, Austin L.

APPLICANT: Gurney, Austin L.

TITLE OF INVENTION: No. US20020123091A1e1 Inhibitor of Hepatocyte Growth Factor Activ TITLE OF INVENTION: No. US20020123091A1e1 Inhibitor of Hepatocyte Growth Factor Activ TITLE OF INVENTION: No. US20020123091A1e1 Inhibitor of Anglogenesis and Cardiovascularization FILE REPRENCE: P1861R1US

CURRENT APPLICATION NUMBER: US/09/742,201

CURRENT FILING DATE: 2000-12-19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ----FCFLEEDPGICRGYITRYFYNQQTKQCERFKY 127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  227 SDHPEDTANVTVTVL-STKQTEDYCLASNKVGRCRGSFPRWYYDPTEQICKSFVYGGCLG 285
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         55; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                46 d----- 84
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2 SEEDEEHTIITDTELPPLKLMHSFCAFKADDGPCRAIMKRFFFNIFTRQCEEFIYGGCEG 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DB 10; Length 513;
                                                                                                            TITLE OF INVENTION: NOVEL PROTEIN, DNA CODING FOR SAME AND METHOD OF PRODUCING THE PROTEIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      68; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                    SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/765,449
FILING DATE: 22-Jan-2001
PRIOR APPLICATION NUMBER: 08/685,558
FILING DATE: CUNKNOWN>
INFORMATION FOR SEQ ID NO: 18
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                        ADDRESSEE: SUGHRUE, MION, ZINN, MACPEAK & SEAS STREET: 2100 Pennsylvania Avenue, N.W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 23.5%; Score 212.5; DB 10
Best Local Similarity 25.5%; Pred. No. 9.9e-14;
Matches 51; Conservative 26; Mismatches 68
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NONRFESLEECKKMC-----TRDNANRIIKTTLQQEK--
                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE DESCRIPTION: SEQ ID NO: 18 US-09-765-449-18
                   APPLICANT: SHIMOMURA, Takeshi
KAWAGUCHI, Toshiya
                                                                                                                                                                                                                                                                                                                                                                        MEDIUM TYPE: Floppy Disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LENGTH: 513 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ORIGINAL SOURCE:
ORGANISM: Homo sapiens
                                                              KITAMURA, Naomi
MIYAZAWA, Keiji
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                406 GGCYGNKNNFEEEQQCLESC 425
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     128 GGCLGNMNNFETLEECKNIC 147
                                                                                                                                                                                                                                                                                                                       ZIP: 20037
COMPUTER READABLE FORM:
                                                                                                                                                             NUMBER OF SEQUENCES: 18
                                                                                                                                                                                       CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                      CITY: Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STRAIN: MKN45
                                                                                                                                                                                                                                                                                                    COUNTRY: USA
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              95
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         δλ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ρp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Q
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              δy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ŏ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               g
```

```
4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          346 CCIDSFLECDDTPNCPDASDEAACEKYTSGFDELQRIHFPSDKGHCVDLPDTGLCKESIP 405
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             227 SDHPEDTANVIVIVI-SIKQTEDYCLASNKVGRCRGSFPRWYXDPTEQICKSFVYGGCLG 285
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         286 NKNNYLREEECILACRGVQGGPLRGSSGAQATFPQGPSMERRHPVCSGTCQPTQFRCSNG 345
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -----FCFLEEDPGICRGYIT 111
                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                    2 SEEDEEHTIITDTELPPLKLMHSFCAFKADDGPCRAIMKRFFFNIFTRQCEEFIYGGCEG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -----TRDNANRIIKTTLQQEK-----
                                                                                                                                                                                                                                                                                                                                                                                                 71;
                                                                                                                                                                                                                                                                                                                                                 Length 529;
                                                                                                                                                                                                                                                                                                                                              22.6%; Score 204.5; DB 10; Length 23.6%; Pred. No. 6.3e-13; Live 26; Mismatches 68; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   112 RYFYNQQTKQCERFKYGGCLGNMNNFETLEECKNIC 147
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRIOR APPLICATION NUMBER: PCT/US00/03565
PRIOR FILING DATE: 2000-02-11
PRIOR APPLICATION NUMBER: PCT/US00/06884
PRIOR FILING DATE: 2000-03-15
PRIOR PLIING DATE: 2000-03-15
PRIOR APPLICATION NUMBER: US 60/253,665
NUMBER OF SEQ ID NOS: 6
SEQ ID NO 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 94 -----PD-----
                                                                                                                                                                                                                                                                                                                                                                            Best Local Similarity 23.6
Matches 51; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              62 NONRFESLEECKKMC--
                                                                                                                                                                                                                                                TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                   US-09-742-201-2
                                                                                                                                                                                                                                                                                                                                                         Query Match
```

Search completed: December 2, 2002, 10:05:19 Job time : 16.2189 secs

```
5.1.3
Compugen Ltd.
 GenCore version
Copyright (c) 1993 - 2002
```

- protein search, using sw model OM protein December 2, 2002, 09:59:55; search time 16.0199 Seconds (without alignments) 416.837 Million cell updates/sec Run on:

US-09-741-106-19

1 DSEEDEEHTIITDTELPPLK......ECKNICEDGPNGFQVDNYGT 161 Perfect score: Sednence:

Scoring table:

BLOSUM62 Gapop 10.0 , Gapext 0.5

112892 segs, 41476328 residues Searched:

112892 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

SwissProt\_40:\* Database : Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

TISSUE=Pancreas;

	P12023 mus musculu Q29428 ovis aries P00994 helix pomat				
IP52_ANESU A4 HUMAN	A4_MOUSE TKD1_SHEEP ISIK_HELPO	IVBI_DENAN SPT3_HUMAN	SBPI_SARBU TKD1_BOVIN	MCPI_MELCP CA36_CHICK	ICS3_BOMMO
	ннн	нη.			-
62	770 265 58	0.09 4.4	164	3137	63
18.5 18.5	18.5 18.4 18.3	18.1	17.8	17.7	17.5
167	167 166.5 166	164	161 160.5	160 160	158
34 35	36 37 38	39	41	4 4 4	45

# ALIGNMENTS

```
P10646; 095103;
01-JUL-1989 (Rel. 11, Last sequence update)
01-JUL-1989 (Rel. 11, Last sequence update)
15-JUL-2002 (Rel. 41, Last annotation update)
Tissue factor pathway inhibitor precursor (TPPI) (Lipoprotein-
associated coagulation inhibitor) (LACI) (Extrinsic pathway inhibitor)
                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A. (ISOFORM ALPHA).
MEDIATE-88198127; PubMed-2452157;
WHUTLY-C., Kretzaner K.K., Girard T.J., Miletich J.P., Broze G.J. Jr.;
"Cloning and characterization of a cDNA coding for the lipoprotein-
associated coagulation inhibitor shows that it consists of three
tandem Kunitz-type inhibitory domains.";
J. Biol. Chem. 263:6001-6004(1988).
                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A. (ISOFORM ALPHA).
MEDINE=91129227; PubMed=1993173;
van der Logt C.P.E., Reitsma P.H., Bertina R.M.;
"Intron-exon organization of the human gene coding for the lipoproteal-associated coagulation inhibitor: the factor Xa dependent inhibitor of the extrinsic pathway of coagulation.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               "Identification of the 1.4 kb and 4.0 kb messages for the lipoprotein associated coagulation inhibitor and expression of the encoded
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A. (ISOFORM ALPHA).
MEDLINE-91161593; PUBMed=2002045;
Girard T.J., Eddy R., Wesselschmidt R.L., Macphail L.A.,
Likert K.M., Byers M.G., Shows T.B., Broze G.J. Jr.;
"Structure of the human lipoprotein-associated coagulation inhibitor enroysome of the organization and localization of the gene to chromosome 2.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Girard T.J., Warren L.A., Novotny W.F., Bejcek B.E., Miletich J.P., Broze G.J. Jr.;
                                                                                                                                                                                                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A. (ISOFORM BETA).
Chang J.-Y., Monroe D.M., Roberts H.R.;
Submitted (AUG-1997) to the EMBL/GenBank/DDBJ databases.
                                   304 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A. (ISOFORM ALPHA).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Biol. Chem. 266:5036-5041(1991).
                                   PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        [6] SEQUENCE FROM N.A. (ISOFORM BETA).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE=89388722; PubMed=2781520;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         hromb. Res. 55:37-50(1989).
                                   STANDARD;
                                                                                                                                                                                        TFPI OR TFPI1 OR LACI.
                                                                                                                                                                                                              Homo sapiens (Human).
                                                                                                                                                                                                                                                                  NCBI_TaxID=9606;
                                 TFPI_HUMAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         protein.
               TFPI_HUMAN
RESULT 1
```

```
This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation-the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -!- SUBCELLULAR LOCATION: Secreted.
-!- ALTERNATIVE PRODUCTS: 2 isoforms; alpha/TFPIalpha (shown here) and beta/TFPIbets, are produced by alternative splicing.
-!- TISSUE SPECIFICITY: MOSTLX IN ENDOTHELIAL CELLS.
-!- DOMAIN: THIS INHIBITOR CONTAINS THREE INHIBITORY DOMAINS.
                                                                                                                                                                                                                                                                                     MEDILINE-66224861; PubMed-8638592;
Nakahara Y., Miyata T., Hamuro T., Funatsu A., Miyagi M.,
Tsunasawa S., Kato H.;
"Amino acid sequence and carbohydrate structure of a recombinant
human tissue factor pathway inhibitor expressed in Chinese hamster
ovary cells: one N-and two O-linked carbohydrate chains are located
between Kunitz domains 2 and 3 and one N-linked carbohydrate chain is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Broze G.J. Jr., Girard T.J., Novotny W.F.; "Regulation of coagulation by a multivalent Kunitz-type inhibitor."; Biochemistry 29:7539-7546(1990).
                                                                                                                                                                                 Girard T.J., Warren L.A., Novotny W.F., Likert K.M., Brown S.G., Miletich J.P., Broze G.J. Jr.; Fructional significance of the Kunitz-type inhibitory domains of lipoprotein-associated coagulation inhibitor."; Nature 338:518-520(1989).
                                                      MEDLINE-90036996; PubMed-2553722;
Novotny W.F., Girard T.J., Miletich J.P., Broze G.J. Jr.;
"purification and characterization of the lipoprotein-associated coaqulation inhibitor from human plasma.";
J. Biol. Chem. 264:18832-18837(1989).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -i- PTM: O-GLYCOSYLATED.
-i- SIMILARITY: CONTAINS 3 BPTI/KUNITZ INHIBITOR DOMAINS.
            Submitted (OCT-2001) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              JOINED.
JOINED.
JOINED.
                                                                                                                                                      INHIBITORY SITES.
MEDLINE-89181950; Pubmed-2927510;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE=91104709; PubMed=2271516;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           JOINED.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        JOINED.
                                                                                                                                                                                                                                                                                                                                                                                                                   Biochemistry 35:6450-6459(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL; J03225; AAA52022.1; -.
EMBL; M58650; AAA59480.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRUCTURE BY NMR OF 121-182.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MS8644; AAA59480.1; MS8645; AAA59480.1; JG
MS8645; AAA59480.1; JG
MS8647; AAA59480.1; JG
MS8648; AAA59480.1; JG
MS8649; AAA59480.1; JG
MS8649; AAA59480.1; JG
                                                                                                                                                                                                                                                                             CARBOHYDRATE-LINKAGE SITES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAA59526.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAA59526.1;
                                                                                                                                                                                                                                                                                                                                                                                                      in Kunitz domain 2
                                          SEQUENCE OF 29-50.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         M58648;
M58649;
M59499;
Strausberg R.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                  REVIEW.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL;
EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL;
EMBL;
EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL;
```

```
EFHGPSWCLTPADRGLCRANENRYYNSVIGKCRPFKYSGC
G -> VTKEGTNDGWKNAAHIYQVFLNAFCIHASMFFLGLD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        99 GNQNRFESLEECKKMCTRDNANRIKTTLQQEKPDFCFLEEDPGICKGYITKYFYNNQTK 148
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  K->I: ABOLISHES INHIBITION OF VII(A)/TF. R->L: ABOLISHES INHIBITION OF X(A). R->L: ABOLISHES INHIBITION OF VII(A)/TF.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   61 GNONRFESLEECKKMCTRDNANRIIKTTLQQEKPDFCFLEEDPGICRGYITRYFYNQQTK 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 DSEEDEEHTIITDTELPPLKLMHSFCAFKADDGPCRAIMKRFFFNIFTRQCEEFIYGGCE 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           88
                                                                                                                                                                                                                                                                                                                                                                                                             SMART; SM00131; KU; 3.
PROSITE; PS00280; BPIL_KUNITZ_1; 3.
PROSITE; PS50279; BPIL_KUNITZ_2; 3.
Serine protease inhibitor; Glycoprotein; Repeat; Blood coagulation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        29 DSEEDEEHTIITDTELPPLKLMHSFCAFKADGPCKAIMKRFFFNIFTRQCEEFIYGGCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     BPTI/KUNITZ INHIBITOR 1
(VII(A)/TISSUE FACTOR BINDING SITE).
BPTI/KUNITZ INHIBITOR 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TISSUE FACTOR PATHWAY INHIBITOR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          REACTIVE BOND (BY SIMILARITY).
N-LINKED (GLCNAC. ..).
O-LINKED.
O-LINKED.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            REACTIVE BOND (BY SIMILARITY).
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
REACTIVE BOND (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 304;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 897; DB 1; Lengtn 50%
Pred. No. 8.5e-79;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Signal; Alternative splicing; 3D-structure; Polymorphism.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (FACTOR X(A) BINDING SITE). BPII/KUNITZ INHIBITOR 3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SISCLC (IN ISOFORM BETA).
MISSING (IN ISOFORM BETA).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               5281E32B758B44FE CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          V -> M (IN DBSNP:5940).
/FTId=VAR_012004.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            N-LINKED (GLCNAC. . .)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   121 QCERFKYGGCLGNMNNFETLEECKNICEDGPNGFQVDNYGT 161
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1; Mismatches
InterPro; IPR002223; Kunitz_BPTI.
Pfam; PF00014; Kunitz_BPTI; 3.
PRINTS; PR00759; BASICPTAGE.
ProDom; PD000222; Kunitz_BPTI; 3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               35015 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     99.1%;
98.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity 98.8
Matches 159; Conservative
                                                                                                                                                                                                                                                                                       Genew; HGNC:11760; TFPI.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   64
135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  304
                                                                                                                                                                                                                                                                    GlycoSuiteDB; P10646;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  64
135
227
304 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           125
                                                                                                                                                                                                                                                                                                              MIM; 152310;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MUTAGEN
MUTAGEN
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ACT_SITE
DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ACT_SITE
DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DISULFID
ACT_SITE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   VARSPLIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            VARSPLIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               VARIANT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MUTAGEN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DOMAIN
        DDRR NODDRR NODDR NODDR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ŏ
```

```
This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation-the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                              15-JUL-1999 (Rel. 38, Created)
15-JUL-1999 (Rel. 38, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
116-OCT pathway inhibitor precursor (TFPI) (Lipoprotein-
associated coagulation inhibitor) (LACI) (Extrinsic pathway inhibitor)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Serine protease inhibitor; Glycoprotein; Repeat; Blood coagulation;
                                                                                                                                                                     Macaca mulatta (Rhesus macaque).
Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (VII(A)/TISSUE FACTOR BINDING SITE).
                                                                                                                                                                                                                                                                                                                                                                                                         -!- SUBCELLULAR LOCATION: Secreted.
-!- DOMAIN: THIS INHIBITOR CONTAINS THREE INHIBITORY DOMAINS.
-!- PTM: O-GLYCOSYLATED (BY SIMILARITY).
-!- SIMILARITY: CONTAINS 3 BPTI/KUNITZ INHIBITOR DOMAINS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TISSUE FACTOR PATHWAY INHIBITOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         BY SIMILARITY.

BY SIMILARITY.

BY SIMILARITY.

REACTIVE BOND (BY SIMILARITY)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
SIMILARITY.
REACTIVE BOND (BY SIMILARITY)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (FACTOR X(A) BINDING SITE). BPII/KUNITZ INHIBITOR 3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       BPTI/KUNITZ INHIBITOR 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               BPTI/KUNITZ INHIBITOR
149 QCERFKYGGCLGNMNNFETLEECKNICEDGPNGFQVDNYGT 189
                                                             304 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        BY SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SIMILARITY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PROSITE; PS00280; BPTI_KUNITZ_1; 3. PROSITE; PS50279; BPTI_KUNITZ_2; 3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Interpro: IPR002223; Kunitz_BPTI.
Pfam: PF00014; Kunitz_BPTI; 3.
PRINTS; PR00759; BASICPTASE.
PRODOM; PD000222; Kunitz_BPTI; 3.
SMART; SM00131; KU; 3.
                                                                                                                                                                                                                                                                     MEDLINE=94375417; PubMed=8089087;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL; S73337; AAB31955.1; -.
                                                                                                                                                                                                          Cercopithecinae; Macaca.
                                                           STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       28
304
104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                100
65
175
175
171
171
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         104
87
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1TFX.
                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                                                                      NCBI_TaxID=9544;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 29
54
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             217
54
63
79
79
125
1125
1135
217
                                                                                                                                                           OR TFPI1
                                                                                                                                                                                                                                                           TISSUE=Liver;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                HSSP; P10646;
                                                           TFPI_MACMU
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ACT_SITE
DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ACT_SITE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Signal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DOMAIN
                                                                       028864
                                               FFPI_MACMU
                                   RESULT 2
 셤
```

```
ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TFPI_RABIT STANDARD; PRT; 300 AA.
P19761, 028828.
01-FBB-1991 (Rel. 17, Created)
01-AUG-1992 (Rel. 23, Last sequence update)
16-OGT-2001 (Rel. 40, Last annotation update)
Tissue factor pathway inhibitor precursor (TFPI) (Lipoprotein-associated coagulation inhibitor) (LACI) (Extrinsic pathway inhibitor)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Belaaouaj A., Kuppuswamy M.N., Birktoft J.J., Bajaj S.P.;
"Revised conA sequence of rabbit tissue factor pathway inhibitor.";
Thromb. Res. 69:547-553(199).
-!- FUNCTION: INHIBITS FACTOR X (X(A)) DIRECTLY AND, IN A XA-DEPENDENT
WAY, INHIBITS VII(A)/TISSUE FACTOR ACTIVITY, PRESUMABLY BY FORMING
A QUATERNARY X(A)/LACI/VII(A)/TF COMPLEX. IT POSSESSES AN
ANTITHROMBOTIC ACTION AND ALSO THE ABILITY TO ASSOCIATE WITH
                                                                                                                                                                                                                                                                                                    61 GNONRFESLEECKKMCTRDNANRIIKTTLQQEKPDFCFLEEDPGICRGYITRYFYNQQTK 120
                                                                                                                                                                              Gaps
                                                                                                                                                                                                             1 DSEEDEEHTIITDTELPPLKLMHSFCAFKADDGPCRAIMKRFFFNIFTRQCEFIYGGCE 60
                                                                                                                                                                                                                                               29 DSEEDBEYTIITDTELPPLKLMHSFCAFKPDDGPCKAIMKRFFFNIFTRQCEEFIYGGCG 88
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Oryctolagus cuniculus (Rabbit).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
                                 REACTIVE BOND (BY SIMILARITY).

N-LINKED (GLCNAC. . .) (POTENTIAL).

N-LINKED (GLCNAC. . .) (POTENTIAL).

N-LINKED (GLCNAC. . .) (POTENTIAL).
                                                                                                                                                                            ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -!- DOMAIN: THIS INHIBITOR CONTAINS THREE INHIBITORY DOMAINS.-!- SIMILARITY: CONTAINS 3 BPTI/KUNITZ INHIBITOR DOMAINS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Warn-Cramer B.J., Broze G.J. Jr., Komives E.A.;
"CDNA sequence of rabbit tissue factor pathway inhibitor.";
Nucleic Acids Res. 20:3548-3548(1992).
                                                                                                                                        92.4%; Score 836; DB 1; Length 304; 91.3%; Pred. No. 5.8e-73; Live 7; Mismatches 7; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Wesselschmidt R.L., Girard T.J., Broze G.J. Jr.;
"CDNA sequence of rabbit lipoprotein-associated coagulation
                                                                                    N-LINKED (GLCNAC. . .) (PO
56E13B3FF16282B0 CRC64;
                                                                                                                                                                                                                                                                                                                                                                          149 QCERFKYGGCLGNMNNFETLEECKNTCEDGLNGFQVDNYGT 189
                                                                                                                                                                                                                                                                                                                                                       121 QCERFKYGGCLGNMNNFETLEECKNICEDGPNGFQVDNYGT 161
 SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Nucleic Acids Res. 18:6440-6440(1990).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LIPOPROTEINS IN PLASMA.
SUBCELLULAR LOCATION: Secreted.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE-91057146; PubMed-2136251;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE=92335027; PubMed=1630940;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  IISSUE=Lung;
MEDLINE=93276427; PubMed=8503123;
250 BY
263 BX
228 RE
145 N-
195 N-
256 N-
35085 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        REVISIONS TO 72; 211 AND 218.
                                                                                                                                                                            Matches 147; Conservative
                                                                                                      304 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
                                                                                                                                                            Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NCBI_TaxID=9986;
 2226
242
2227
2227
1195
256
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TISSUE=Liver;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      inhibitor.
              DISULFID
ACT_SITE
CARBOHYD
CARBOHYD
                                                                                    CARBOHYD
                                                                                                                                         Query Match
                                                                                                                                                              Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LISSUE=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                TFPI_RABIT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STEEFF
                                                                                                                                                                                                                                                                                   δλ
                                                                                                                                                                                                                                                                                                                    g
                                                                                                                                                                                                                                                                                                                                                       Qγ
                                                                                                                                                                                                                                                                                                                                                                                        d
                                                                                                                                                                                                               οχ
```

```
;
0
the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TrPI_RAT STANDARD; PRT; 302 AA.

002445.

01-JUL-1993 (Rel. 26, Last sequence update)

01-JUL-1993 (Rel. 26, Last annotation update)

16-OCT-2001 (Rel. 40, Last annotation update)

Tissue factor pathway inhibitor precursor (TPPI) (Lipoprotein-associated coagulation inhibitor) (LACI) (Extrinsic pathway inhibitor)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  62 NONRFESLEECKKMCTRDNANRIIKTTLQQEKPDFCFLEEDPGICRGYITRYFYNQQTKQ 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SMART; SM00131; KU; 3. CONTINE 1; 3. PROSITE; PS00280; BPTL KUNITZ 1; 3. PROSITE; PS50279; BPTL KUNITZ 2; 3. Serine protease inhibitor; Glycoprotein; Repeat; Blood coagulation;
                                                                                                                                                                                                                                                                                                                                                                                                                           BY SIMILARITY.

N-LINED (GLCNAC. ...) (POTENTIAL).

N-LINED (GLCNAC. ...) (POTENTIAL).

N-LINED (GLCNAC. ...) (POTENTIAL).

N-LINED (GLCNAC. ...) (POTENTIAL).

MISSING (IN REF. 3).

PKSI -> RMLS (IN REF. 3).

PKSI -> RMLS (IN REF. 3).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEEDEEHTIITDTELPPLKLMHSFCAFKADDGPCRAIMKRFFFNIFTROCEEFIYGGCEG
                                                                                                                                                                                                                                                                                        BPTI/KUNITZ INHIBITOR 1
(VII(A)/TISSUE FACTOR BINDING SITE).
BPTI/KUNITZ INHIBITOR 2
                                                                                                                                                                                                                                                                             TISSUE FACTOR PATHWAY INHIBITOR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       e 658; DB 1; Length 300; No. 6.2e-56;
                                                                                                                                                                                                                                                                                                                                                                       BY SIMILARITY.

BY SIMILARITY.

BY SIMILARITY.

REACTIVE BOND (BY SIMILARITY)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Best Local Similarity 73.1%; Pred. No. 6.2e-56;
Matches 117; Conservative 13; Mismatches 30; Indels
                                                                                                                                                                                                                                                                                                                                (FACTOR X(A) BINDING SITE).
BPTI/KUNITZ INHIBITOR 3
(BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       146 CERFKYGGCLGNLNNFESLEECKNTCENPTSDFQVDDHRT 185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         122 CERFKYGGCLGNMNNFETLEECKNICEDGPNGFQVDNYGT 161
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       72.7%; Score 658;
73.1%; Pred. No. 6
                                                                               EMBL; X54708; CAA38515.1; ALT_SEQ.
EEMBL; SG1902; AAB26836.1; -.
PIR; S12143; S12143.
HSSP; P10646; ITFX.
                                                                                                                                    InterPro; IPR002223; Kunitz_BPTI.
Pfam; PF00014; Kunitz_BPTI; 3.
PRINTS; PR00759; BASICPTASE.
PRODOM; PD000222; Kunitz_BPTI; 3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              34435 MW;
                                                                                                                                                                                                                                                              24
300
100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  246
259
224
141
191
252
272
                                                                                                                                                                                                                                                                                                                     171
                                                                                                                                                                                                                                                                                                                                                                                       83
96
61
171
171
1154
1167
1132
263
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    31
269
300 AA;
                                                                                                                                                                                                                                                                 25
50
                                                                                                                                                                                                                                                                                                                                               213
                                                                                                                                                                                                                                                                                                                   121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CONFLICT
CONFLICT
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                   DISULFID
ACT_SITE
DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ACT_SITE
DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ACT_SITE
CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                            DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
                                                                                                                                                                                                                                                                                                                                                                          DISULFID
                                                                                                                                                                                                                                                                                                                                                                                         DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CARBOHYD
                                                                                                                                                                                                                                                                SIGNAL
                                                                                                                                                                                                                                                                                          DOMAIN
                                                                                                                                                                                                                                                    Signal
                                                                                                                                                                                                                                                                                                                     DOMAIN
                                                                                                                                                                                                                                                                                                                                                DOMAIN
                                                                                                                                                                                                                                                                             CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 4
TFPI_RAT
  셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   δ
```

```
This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its way non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@lsb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ó:
                                                                                                                                                 (TFPI).";
J. Biochem. 111:681-687(1992).
J. Biochem. INHIBITS FACTOR X (X(A)) DIRECTLY AND, IN A XA-DEPENDENT
-!- FUNCTION: INHIBITS YII(A)/TISSUE FACTOR ACTIVITY, PRESUMABLY BY FORMING
A QUATERNARY X(A)/LACI/VII(A)/TF COMPLEX. IT POSSESSES AN
ANTITHROMBOTIC ACTION AND ALSO THE ABILITY TO ASSOCIATE WITH
                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SMART; SM00131; KU; 3.
PROSTEE; PS00280; BPTL KUNITZ_1; 3.
PROSITE; PS50279; BPTL KUNITZ_2; 3.
Serine protease inhibitor; Glycoprotein; Repeat; Blood coagulation;
                                                                                         STRAIN-Sprague-Dawley; TISSUE-Liver;
MEDILNE-9248861; pubmed-1639767;
Enjyoji K.-I., Emi M., Mukai T., Kato H.;
"CDNA cloning and expression of rat tissue factor pathway inhibitor
                                                                                                                                                                                                                                 LIPOPROTEINS IN PLASMA.
--- SUBCELLULAR LOCATION: Secreted.
--- TISSUE SPECIFICITY: MOST ABUNDANT IN HEART, LUNG, KIDNEY, AND AORTIC ENDOTHELLAL CELLS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TISSUE FACTOR PATHWAY INHIBITOR.
BPTI/KUNITZ INHIBITOR 1
(VII(A)/TISSUE FACTOR BINDING SITE).
BPTI/KUNITZ INHIBITOR 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
AND SIMILARITY.
N-LINKED GLCNAC. .) (POTENTIAL).
N-LINKED (GLCNAC. .) (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               201 N-LINKED (GLCNAC. . .) (POTENTIAL)
34554 MW; F9AEB2130A24A59F CRC64;
                                                                                                                                                                                                                                                                                    -i- DOMAIN: THIS INHIBITOR CONTAINS THREE INHIBITORY DOMAINS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            REACTIVE BOND (BY SIMILARITY).
BY SIMILARITY
BY SIMILARITY.
BY SIMILARITY.
REACTIVE BOND (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 302;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    31; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (FACTOR X(A) BINDING SITE). BPII/KUNITZ INHIBITOR 3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        65.6%; Score 594; DB 1; 63.9%; Pred. No. 8.3e-50; ive 26; Mismatches 31;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   HSSP; P10646; ITFX.
InterPro; IPR002223; Kunitz_BPTI.
Infem; PF00014; Kunitz_BPTI; 3.
PRINTS; PR00759; BASICPTASE.
ProDom; PD000222; Kunitz_BPTI; 3.
                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL; D10926; BAA01724.1; -. PIR; JX0213; TIRTGK.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
            norvegicus (Rat).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2272
1033
86
99
1174
1170
1170
1135
2272
2272
2255
2255
2333
251
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          28
302
103
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        144
251
261
302 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Local Similarity
nes 101; Conserv
                                                                               SEQUENCE FROM N.A.
                                                     NCBI_TaxID=10116;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1
29
53
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          222
53
62
78
78
63
124
149
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ACT_SITE
DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ACT_SITE
DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ACT_SITE
CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Signal.
SIGNAL
            Rattus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Matches
```

à

(EPI),

```
PROSITE; PS50279;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT
  q
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      q
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                δy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             òλ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE=99138770; PubMed=9974373;

Chang J.-Y., Monroe D.M., Oliver J.A., Roberts H.R.;

Chang J.-Y., Monroe D.M., Oliver J.A., Roberts H.R.;

TPFDbeta, a second pare ";

Inhibitor (TPPI) gene.";

Thromb. Haemost. 81:45-49(1.999).

-!- FUNCTION: INHIBITS FACTOR X (X(A)) DIRECTLY AND, IN A XA-DEPENDENT WAY, INHIBITS YII(A)/TISSUE FACTOR ACTIVITY, PRESUMABLY BY FORMING A QUATERNARY X(A)/LACI/VII(A)/TF COMPLEX. IT POSSESSES AN ANTITHROMBOTIC ACTION AND ALSO THE ABILITY TO ASSOCIATE WITH LIPOPROTEINS IN PLASAMA (BY SIMILARITY).

-!- ALTERNATIVE PRODUCTS: 2 isoforms; alpha/TFPIalpha (shown here) and beta/TFPIDeta; are produced by alternative splicing.

-!- ALTERNATIVE PRODUCTS: 1 isoform alpha is expressed in heart and beta/TFPIDETCHY: Isoform alpha is expressed in heart and lung.

-!- SUBMELLICITY: Isoform beta in heart and lung.

-!- SUBMELLICITY: CONTAINS 3 BPTI/KUNITZ INHIBITOR DOMAINS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bloinformatics and the EMBL outstation-the Buropean Bloinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way madified and this statement is not removed. Usage by and for commercial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     16-OCT-2001 (Rel. 40, Last sequence update)
15-UN-2002 (Rel. 41, Last annotation update)
15-Save factor pathway inhibitor precursor (FFPI) (Lipoprotein-associated coagulation inhibitor) (LACI) (Extrinsic pathway inhibitor)
                                                                                  NRFESLEECKKMCTRDNANRIIKTTLQQEKPDFCFLEEDPGICRGYITRYFYNQQTKQCE 123
                                                                                                                                     NRFDTLEECRKTCIPGYKKTTIKTTSGAEKPDFCFLEEDPGICRGFMTRYFYNNOSKOCE 150
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Chang J. Y., Monroe D.M., Oliver J.A., Liles D.K., Roberts H.R.; "Cloning, expression, and characterization of mouse tissue factor pathway inhibitor (TFPI)."; Thromb. Haemost. 79:306-309(1998).
                                                                                                                                                                                                                        RFKYGGCLGNMNNFETLEECKNICEDGPNGFQVDNYGT 161
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      [1]
SEQUENCE FROM N.A. (ISOFORM ALPHA).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SMART; SM00131; KU; 3.
PROSITE; PS00280; BPTI_KUNITZ_1; 3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      [2]
SEQUENCE FROM N.A. (ISOFORM BETA).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MGD: MGI:1095418; Tfpi.
InterPro: IPR00223; Kunitz_BPTI.
Pfam; PF00014; Kunitz_BPTI; 5.
PRINTS; PR00759; BASICPTASE.
ProDom; PD000222; Kunitz_BPTI; 3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE=98152575; PubMed=9493581;
                                                                                                                                                                                                                                                                                                                                                      EMBL; AF004833; AAC40035.1; -. EMBL; AF016313; AAD01586.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mus musculus (Mouse).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     P10646; 1TFX.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STRAIN-129
                                                                                                                                                                                                                                                                                                                                                           TFPI_MOUSE
                                                                                  64
                                                                                                                                                                                                                                                                                                                                    RESULT
                                                                                                                                                                                                                                                                                                                                                                                                                 DATE THE TOTAL THE TARKET AND THE TOTAL THE TARKET AND THE TOTAL THE TARKET AND T
                               Dβ
                                                                                  δ
                                                                                                                                     pp
                                                                                                                                                                                              ò
                                                                                                                                                                                                                                               q
```

```
62 NONRFESLEECKKMCTRDNANRIIKTTLQQEKPDFCFLEEDPGICRGYITRYFYNQQTKQ 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Ļ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             85
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TKEETNGGWKNADYTYQGFLSSVYIHVLYFVFRIG (IN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2 SEEDEEHTIITDTELPPLKLMHSFCAFKADDGPCRAIMKRFFFNIFTRQCEEFIYGGCEG 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Miyagi Y., Koshikawa N., Yasumitsu H., Miyagi E., Hirahara F., Aoki I., Misugi K., Umeda M., Miyazaki K.; "CDNA cloning and mRNA expression of a serine proteinase inhibitor secreted by cancer cells: identification as placental protein 5 and tissue factor pathway inhibitor-2.";
                       Serine protease inhibitor; Glycoprotein; Repeat; Blood coagulation; Signal; Alternative splicing.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
REACTIVE BOND (BY SIMILARITY).
N-LINKED (GLCNAC. .) (POTENTIAL).
N-LINKED (GLCNAC. .) (POTENTIAL).
N-LINKED (GLCNAC. .) (POTENTIAL).
N-LINKED (GLCNAC. .) (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DYRGRPWCLQPADSGLCKASERRFYYNSATGKCHRF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                    BPTI/KUNITZ INHIBITOR 1
(VII(A)/TISSUE FACTOR BINDING SITE)
BPTI/KUNITZ INHIBITOR 2
(FACTOR X(A) BINDING SITE).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-FEB-1996 (Rel. 33, Created)
01-FEB-1996 (Rel. 33, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Tissue factor pathway inhibitor 2 precursor (TFPI-2) (Placental protein 5) (PP5).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   10;
                                                                                                          TISSUE FACTOR PATHWAY INHIBITOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 1; Length 306;
                                                                                                                                                                                                                                                                                                                                                                    REACTIVE BOND (BY SIMILARITY)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   32; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     122 CERFKYGGCLGNMNNFETLEECKNICED-----GP-NGFQVDNYGT 161
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  146 CERFUYGGCLGNRNNFETLDECKKICENPUHSPSPVNEVQMSDYUT 191
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MISSING (IN ISOFORM BETA).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                D3EA3297E4B6A359 CRC64;
                                                                                                                                                                                                                                                 BPTI/KUNITZ INHIBITOR 3.
                                                                                                                                                                                                                                                                                                                                                                                            BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
REACTIVE BOND (BY S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; Score 563; DB 1;
; Pred. No. 7.8e-47;
24; Mismatches 32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (IN REF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       235 AA
                                                                                                                                                                                                                                                                                                         BY SIMILARITY.
BY SIMILARITY.
                                                                                                                                                                                                                                                                                 SIMILARITY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   BETA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ISOFORM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRT;
BPTI_KUNITZ_2; 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TISSUE=Placenta;
MEDLINE=95204397; PubMed=7896752;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   34987 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           62.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  60.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Best Local Similarity 60.29
Matches 100; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           306
68
                                                                                                          306
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Homo sapiens (Human).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   306 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NCBI_TaxID=9606;
                                                                                                          29
                                                                                                                                                                                                                                                    TFP2_HUMAN P48307;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           VARSPLIC
CONFLICT
                                                                                                                                                                                                                                                                                                                                                                    ACT_SITE
DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ACT_SITE
DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ACT_SITE CARBOHYD
                                                                                                                                                                                                                                                                                 DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CARBOHYD
CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                    DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CARBOHYD
                                                                                                                                                                                                                                                                                                                                         DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                            DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           VARSPLIC
                                                                                                                                          DOMAIN
                                                                                  SIGNAL
                                                                                                                                                                                               DOMAIN
                                                                                                                                                                                                                                                       DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FPPI2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TFP2_HUMAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ID DATE OF THE STATE OF THE STA
```

3;

```
δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the PRBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (see http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Buctzow R., Huhtala M.-L., Bohn H., Virtanen I., Seppaelae M.;
Biochem. Biophys. Res. Commun. 151:650-631(1988).

-!- FUNCTION: SEEMS TO INHIBIT TRYPSIN, FACTOR VII(A)/TISSUE FACTOR,
WEAKLY FACTOR XA. HAS NO EFFECT ON THROMBIN.

-!- SUBCELLULAR LOCATION: Secreted.

-!- TISSUE SPECIFICITY: UMBILICAL VEIN ENDOTHELIAL CELLS, LIVER,
PLACENTA, HEART, PANCREAS, AND MATERNAL SERUM AT ADVANCED
PREGNANCY.
                                                                                                                                                                                                  PubMed=1134222;
Mamei S., Kazama Y., Kuijper J.L., Foster D.C., Kisiel W.;
"Genomic structure and promoter activity of the human tissue factor
pathway inhibitor-2 gene.";
                                                               Sprecher C.A., Kisiel W., Mathewes S., Foster D.C., "Molecular cloning, expression, and partial characterization of second human tissue-factor-pathway inhibitor."; Proc. Natl. Acad. Sci. U.S.A. 91:3353-3357(1994).
                                                                                                                                                                                                                                                                                                                                                                                     Buetzow R., Huhtala M.-L., Bohn H., Virtanen I., Seppaelae M.,
"Purification and characterization of placental protein 5.";
Blochem. Biophys. Res. Commun. 150:483-490(1988).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DOMAIN: THIS INHIBITOR CONTAINS THREE INHIBITORY DOMAINS.
SIMILARITY: CONTAINS 3 BPTI/KUNITZ INHIBITOR DOMAINS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PROSITE; PS00280; BPTI_KUNITZ_1; 2.
PROSITE; PS50279; BPTI_KUNITZ_2; 3.
Serine protease inhibitor; Glycoprotein; Repeat; Signal;
Blood coagulation; Polymorphism.
                                                                                                                                                                                                                                                                                                        Strausberg R.; Submitted (MAR-2001) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                         Submitted (MAY-1997) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                              PARTIAL SEQUENCE OF 23-35; 47-53 AND 133-146.
                                                                                                                                                                                                                                                    Biochim. Biophys. Acta 1517:430-435(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Interpro: IPR002233; Kunitz_BPTI.
Pfam; PF00014; Kunitz_BPTI; 3.
PRINTS; PR00759; BASICPTASE.
ProDom; PD000222; Kunitz_BPTI; 3.
                                      TISSUE=Placenta;
MEDLINE=94211862; PubMed=8159751;
                                                                                                                                                                                                                                                                                                                                                                          MEDLINE-88106628; PubMed-3276312;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL; D29992; BAA06272.1; -.
EMBL; L27624; AAA20094.1; -.
EMBL; AC002076; AAB54049.1; -.
EMBL; AF217542; AAR13254.1; -.
EMBL; BC005330; AAH05330.1; -.
Biochem. 116:939-942(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Genew; HGNC:11761; TFPI2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PIR, A34029, A34029.
PIR, B34029, B34029.
PIR, C34029, C34029.
HSSP, P12111, 1KNT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SMART; SM00131; KU; 2
                                                                                                                                                                                    SEQUENCE EROM N.A.
                          SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
                                                                                                                               SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                             TISSUE-Placenta;
                                                                                                                                                                                                                                                                                             TISSUE=Brain;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          600033;
                                                                                                                                                                                                                                                                                                                                                                                                                                           ERRATUM.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MIM;
```

```
3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
STRAIN=CRF, TISSUE-Placenta;
MEDLINE=97101108; PubMed=8945635;
Miyagi Y., Yasumitsu H., Mizushima H., Koshikawa N., Matsuda Y.,
Itoh H., Hori T., Aoki I., Misugi K., Miyazaki K.;
"Cloning of the cDNA encoding mouse PP5/TFPI-2 and mapping of the gene to chromosome 6.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Kazama Y., Kamei S., Kuijper J., Foster D.C., Kisiel W.;
"Nucleotide sequence of the gene encoding murine tissue factor pathway
inhibitor-2.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      96 CRLQVSVDDQCEGSTEKYFFNLSSMTCEKFFSGGCHRNRIENRFPDEATCMGFCAPKKIP 155
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 51; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    36 CLLPLDYGPCRALLLRYYYDRYTQSCRQFLYGGCEGNANNFYTWEACDDACWRIEKVPKV 95
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           26 CAFKADDGPCRAIMKRFFFNIFTRQCEEFIYGGCEGNQNRFESLEECKKMCTR-DNANRI 84
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              85 IK-----P 94
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Submitted (AUG-1999) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: SEEMS TO INHIBIT TRYPSIN, FACTOR VII(A)/TISSUE FACTOR, WEAKLY FACTOR XA. HAS NO EFFECT ON THROMBIN.
                                                                                                                    REACTIVE BOND (BY SIMILARITY).
REACTIVE BOND (BY SIMILARITY).
REACTIVE BOND (BY SIMILARITY).
BY SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalla, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
                    FACTOR PATHWAY INHIBITOR 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 95 DFCFLEEDPGICRGYITRYFYNQQTKQCERFKYGGCLGNMNNFETLEECKNIC 147
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DB 1; Length 235;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      30.3%; Score 274.5; DB 1; Length; 28.9%; Pred. No. 2.4e-19; Live 29; Mismatches 43; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                         V -> A (IN DBSNP:1804202).
/FIId=VAR 012005.
D -> A (IN REF. 6).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -> A (IN REF. 6).
975ABA5C53F7C65F CRC64;
                    TISSUE FACTOR PATHWAY INF
BPTI/KUNITZ INHIBITOR 1.
BPTI/KUNITZ INHIBITOR 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      16-00T-2001 (Rel. 40, Created)
16-0CT-2001 (Rel. 40, Last sequence update)
16-0CT-2001 (Rel. 40, Last annotation update)
Tissue factor pathway inhibitor 2 precursor (TFPI-2).
                                                                                  BPTI/KUNITZ INHIBITOR 3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  230 AA.
                                                                                                         POLY-LYS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DNA Cell Biol. 15:947-954(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          23 D
26934 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Best Local Similarity 28.9
Matches 50; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STANDARD;
22
86
86
1449
86
108
87
147
148
149
149
110
110
110
110
110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          23
235 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TFP2_MOUSE 035536;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CONFLICT
                                                                                                                             ACT_SITE
ACT_SITE
                                                                                                                                                                       ACT_SITE
DISULFID
                                                                                                                                                                                                                                                                                                                      DISULFID
                                                                                                                                                                                                                  DISULFID
                                                                                                                                                                                                                                    DISULFID
                                                                                                                                                                                                                                                            DISULFID
                                                                                                                                                                                                                                                                                DISULFID
                                                                                                                                                                                                                                                                                                       DISULFID
                                                                                                                                                                                                                                                                                                                                                                 DISULFID
                                                                                                                                                                                                                                                                                                                                                                                         CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                              CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                  VARIANT
                                            DOMAIN
                                                              DOMAIN
                                                                                       DOMAIN
                                                                                                           DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TFP2_MOUSE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 7
```

```
g
δλ
                                                  This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its was by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           156 CSSPKDEGLCSANVTRFYFNSRNKTCETFTYTGCGGNENNFYYLDACHRACVKGWKKPKR 215
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         96 CRSELKTYPCDKPNIRFFFNLNTMTCEPLRPGLCSRTINVFSEEATCKGLCEPRKHIPSF 155
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              97 CFLEEDPGICRGYITRYFYNQQTKQCERFKYGGCLGNMNNFETLEECKNICEDG---PNG 153
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         26 CAFKADDGPCRAIMKRFFFNIFTRQCEEFIYGGCEGNQNRFESLEECKKMCTR----- 78
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    79 -----DNAN------DDF 96
          SPECIFICITY: HIGHLY EXPRESSED IN PLACENTA. ALSO EXPRESSED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   N-LINKED (GLCNAC. . .) (POTENTIAL)
N-LINKED (GLCNAC. . .) (POTENTIAL)
                                                                                                                                                                                                                                                                                              BY SIMILARITY.
TISSUE FACTOR PATHWAY INHIBITOR 2.
                                                                                                                                                                                                                                                                                                                                                 REACTIVE BOND (BY SIMILARITY).
REACTIVE BOND (BY SIMILARITY).
BY SIMILARITY.
                  IN LIYER AND KIDNEY.
DOMAIN: THIS INHIBITOR CONTAINS THREE INHIBITORY DOMAINS.
SIMILARITY: CONTAINS 3 BPTI/KUNITZ INHIBITOR DOMAINS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            26.7%; Score 242; DB 1; Length 230; 26.9%; Pred. No. 3e-16; tive 27; Mismatches 57; Indels
                                                                                                                                                                                                                                                   PROSITE; PS00280; BPTI_KUNITZ_1; 2.
PROSITE; PS50279; BPTI_KUNITZ_2; 3.
Serine protease inhibitor; Glycoprotein; Repeat; Signal;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         57EADB2E36521C7B CRC64;
                                                                                                                                                                                                                                                                                                                    BPTI/KUNITZ INHIBITOR 1.
BPTI/KUNITZ INHIBITOR 2.
BPTI/KUNITZ INHIBITOR 3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRT; 1416 AA.
SUBCELLULAR LOCATION: Secreted
                                                                                                                                                                        HSSP; P12111; 1KNT.
MGD; MGI:108543; Tfp12.
InterPro; 1PR002223; Kunitz_BPTI.
Pfam: PF00014; Kunitz_BPTI; 3.
PRINTS; PR00759; BASICPTASE.
ProDom; PD000222; Kunitz_BPTI; 2.
                                                                                                                                                                EMBL; AF180353; AAF40412.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         26137 MW;
                                                                                                                                                    EMBL; D50586; BAA22585.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   50; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                             105
121
156
156
165
181
281
178
178
                                                                                                                                                                                                                                          SMART; SM00131; KU;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Best Local Similarity
                                                                                                                                                                                                                                                                                      Blood coagulation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         154 FQVDNY 159
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        216 WKIGDF 221
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    YN81_CAEEL
Q03610;
                                                                                                                                                                                                                                                                                                                                         DOMAIN
ACT_SITE
ACT_SITE
ACT_SITE
DISULFID
                                                                                                                                                                                                                                                                                                                                                                                             DISULFID
DISULFID
DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                             DISULFID
DISULFID
DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CARBOHYD
CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                               DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE
                                                                                                                                                                                                                                                                                                                     DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT 8
YN81_CAEEL
                                                                                                                                                                                                                                                                                                SIGNAL
                                                                                                                                                                                                                                                                                                           CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Matches
g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   염
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         δλ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               q
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   õ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ò
```

```
This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                  STRAINEERISCOLNZ;
MEDLINE=94150718; Pubbled=7906398;
MEDLINE=94150718; Pubbled=7906398;
Milson R., Ainscough R., Anderson K., Baynes C., Berks M.,
Bonfield J., Button J., Connell M., Copsey T., Cooper J., Coulson A.,
Craxton M., Dear S., Du Z., Durbin R., Favello A., Fraser A.,
Fulton L., Gardner A., Green P., Hawkins T., Hillact L., Jier M.,
Johnston L., Jones M., Kershaw J., Kairsten J., Laisster N.,
Latreille P., Lightning J., Lloyd C., Mortimore B., O'Callaghan M.,
Parsons J., Percy C., Rifken L., Roopra A., Saunders D., Shownkeen R.,
Sims M., Smaldon N., Smith A., Smith M., Sonnhammer E., Staden R.,
Sulston J., Thierry-Mieg J., Thomas K., Vaudin M., Vaughan K.,
Waterston R., Watson A., Weinstock L., Wilkinson-Sproat J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     24 SFCAFKADDGPCRAIMKRFFFNIFTRQCEEFIYGGCEGNQNRFESLEECKKMCTRDNANR 83
                                                                                                                                                                                                     Eukaryota, Metazoa, Nematoda, Chromadorea, Rhabditida, Rhabditoidea,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "2.2 Mb of contiguous nucleotide sequence from chromosome III of C. elegans.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   54; Indels 41;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          26.7%; Score 241.5; DB 1; Length 1416; 33.1%; Pred. No. 2.2e-15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Jones S.J.M.;
Submitted (NOV-1997) to the EMBL/GenBank/DDBJ databases.
-!- SIMILARITY: STRONG, TO D1044.3.
-!- SIMILARITY: CONTAINS 5 BPTI/KUNITZ INHIBITOR DOMAINS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PROSITE; PS00260; BPTL_KUNITZ_1; 3.
PROSITE; PS50279; BPTL_KUNITZ_2; 5.
PROSITE; PS50186; EGF_2; UNKNUM_1.
Hypothetical protein; Serine protease inhibitor; Repeat.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            152986 MW; 531CACE1CB22F70D CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     BPTI/KUNITZ INHIBITOR I.
BPTI/KUNITZ INHIBITOR 2.
BPTI/KUNITZ INHIBITOR 3.
BPTI/KUNITZ INHIBITOR 4.
BPTI/KUNITZ INHIBITOR 4.
01-FEB-1994 (Rel. 28, Created)
15-JUL-1998 (Rel. 36, Last Sequence update)
15-JUL-2002 (Rel. 41, Last annotation update)
Hypothetical protein ZC84.1 in chromosome III
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   18; Mismatches
                                                                                                                                                                                                                   Rhabditidae; Peloderinae; Caenorhabditis.
NCBI_TaxID=6239;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL; 219157; CAA79569.1; -. PIR; 528291; S28291. S28291. HSSP; P000974; IPAK. WORMPEP; 2CG4.1; CE15020. InterPro; IPR000561; EGF-like. InterPro; IPR000253; Kunitz_BPTI. InterPro; IPR00259; WAI/EB. Ffam; PF00014; Kunitz_BPTI; 5. Pfam; PF01683; EB; 3.__BPTI; 5.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRINTS; PR00759; BASICPTASE.
ProDom; PD000222; Kunitz_BPTI; 5.
SMART; SM00131; KU; 5.
SMART; SM00289; WRI; 13.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   56; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           484
590
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Nature 368:32-38(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                698
                                                                                                                                                                          Caenorhabditis elegans.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1416 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Wohldman P.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    REVISIONS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Matches
```

ŝ

Mon Dec

```
MEDINE-84133808; Pubmed-6199276;
Hochstrasser K., Albrecht G.J., Schoenberger O.L., Wachter E.;
Hochstrasser K., Albrecht G.J., Schoenberger O.L., Wachter E.;
"Kunitz-type proteinase inhibitors derived by limited proteolysis of
the inter-alpha-trypsin inhibitor. VII. Characterization of the
bovine inhibitor as double-headed trypsin-elastase inhibitor.";
Hoppe-Seyler's Z. Physiol. Chem. 364:1689-1696(1983).
-!- FUNCTION: ALPHA-1-MICROGLOBUIN OCCURS IN MANY PHYSIOLOGICAL
FULUDS INCLUDING PLASHA, URINE, AND CERBEROSFINAL FLUID. IT
APPEARS NOT ONLY AS A FREE MONOMER BUT ALSO IN COMPLEXES WITH IGA
                                                                                                                                                                                                                             AMBP_BOVIN STANDARD; PRT; 352 AA.
P00978: P55420; Q28020;
21-JUL-1986 (Rel. 0). Created)
21-JUL-1997 (Rel. 35, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
AMBP protein precursor (Contains: Alpha-1-microglobulin; Inter-alpha-trypsin inhibitor light chain (ITI-LC) (Bikunin) (HI-30)
Cumulus extracellular matrix stabilizing factor) (ESF)].
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Lindqvist A., Aakerstroem B.; "Bolation and characterization and characterization and union and union and of liver cDNA and urinary alpha 1-microglobulin."; Biochim. Biophys. Acta 1306:98-106(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Hochstrasser K., Wachter E., Albrecht G.J., Reisinger P., "Kunitz-type proteinase inhibitors derived by limited proteolysis of the inter-alpha-trypsin inhibitor, X. The amino-acid sequences of the trypsin released inhibitors from horse and pig inter-alpha-trypsin inhibitors.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TISSUE-Fetal serum;
MEDLINE-92291130; PubMed-1376324;
Chen L., Mao S.J.T., Larsen W.J.;
"Identification of a factor in fetal bovine serum that stabilizes the cumulus extracellular matrix. A role for a member of the inter-alphatrypsin inhibitor family.";
J. Biol. Chem. 267:12380-12386(1992).
-- CFLEEDPGI-C- 106
                                        490 EPKCIQGQAYKDMFGNFVTCSNGMGCPANYECYFDGSQWGCCPTKAFTCSLNTDSGIQCG 549
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Kunitz-type proteinase inhibitors derived by limited proteolysis of
                                                                                                                                                                                                                                                                                                                                                                                                                           Bos taurus (Bovine).
Bukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Butheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
Bovidae; Bovinae; Bos.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      the inter-alpha-trypsin inhibitor, VII. Determination of the amino-acid sequence of the trypsin-released inhibitor from bovine inter-alpha-trypsin inhibitor.";
Hoppe-Seyler's Z. Physiol. Chem. 364:1679-1687(1983).
                                                                                                         107 RGYITRYFYNQQTKQCERFKYGGCLGNMNNFETLEECKNICEDG--PNG 153
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Biol. Chem. Hoppe-Seyler 366:473-478(1985).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE OF 227-349.
MEDLINE-85225967; PubMed=2408637;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE-84133807; PubMed-6199275;
Hochstrasser K., Wachter E.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE=96201710; PubMed=8611630;
84 IIKTTLQQEKPDF--------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE OF 227-348.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE OF 206-219.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NCBI_TaxID-9913;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AND ALBUMIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             REACTIVE SITES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TISSUE-Liver;
                                                                                                                                                                                                               AMBP_BOVIN
                                                                                                                                                                                         RESULT 9
                                                                                  ò
```

```
This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                           STIMULUS TO ACT AS STRUCTURAL LINKER THAT ENSURE NORMAL CUMULUS EXPANSION, THROUGH STABILIZATION OF THE CUMULUS EXTRACELLULAR MATRIX THUS SUPPORTING THE PROCESS OF OVULATION.
SUBDIT: I-ALPHA-I plasma protease inhibitors are assembled from one or two heavy chains (H1, H2 or H3) and one light chain, bikunin. Inter-alpha-inhibitor (I-ALPHA-I) is composed of H1, H2 and bikunin, inter-alpha-like inhibitor (I-ALPHA-LI) of H2 and bikunin, and pre-alpha-inhibitor (P-ALPHA-LI) of H3 and bikunin (By
                                                                                                                                                                                                                                                  -!- FTM: The precursor is proteolytically processed into two separately functioning proteins.
-!- PTM: Alpha-1-microglobulin contains covalently linked brown-yellow chromophores (By similarity).
-!- SIMILARITY: IN THE N-TERMINAL SECTION; BELONGS TO THE LIPOCALIN
FUNCTION: INTER-ALPHA-TRYPSIN INHIBITOR, PRESENT IN PLASMA AND
                               ELASTASE.
FUNCTION: MAY DIFFUSE INTO FOLLICULAR FLUID AFTER AN OVULATORY
                URINE, INHIBITS TRYPSIN, PLASMIN, AND LYSOSOMAL GRANULOCYTIC
                                                                                                                                                                                     similarity).
SUBCELLULAR LOCATION: Secreted.
TISSUE SPECIFICITY: Synthesized in the liver and secreted in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            N-LINKED (GLCNAC. ..) (POTENTIAL).
N-LINKED (GLCNAC. ..) (POTENTIAL).
N-LINKED (GLCNAC. ..).
T -> G (IN REF. 4).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            INTER-ALPHA-TRYPSIN INHIBITOR LIGHT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                INHIBITORY SITE (P1) (CHYMOTRYPSIN, ELASTASE).
INHIBITORY SITE (P1) (TRYPSIN).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Glycoprotein; Plasma; Signal; Serine protease inhibitor; Repeat;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        BPTI/KUNITZ INHIBITOR 1.
BPTI/KUNITZ INHIBITOR 2.
CHROMOPHORE (BY SIMILARITY).
CHROMOPHORE (BY SIMILARITY).
CHROMOPHORE (BY SIMILARITY).
CHROMOPHORE (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                -!- SIMILARITY: CONTAINS 2 BPTI/KUNITZ INHIBITOR DOMAINS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MICROGLOBULIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   BY SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRINTS; PRO0759; BASICPTASE.
PRINTS; PRO0179; LIPOCALIN.
ProDom; PD000022; Kunitz_BPT; 2.
SMART; SM00131; KU; 2.
PROSITE; PS00280; BPTI KUNITZ_1; 2.
PROSITE; PS00213; LIPOCALIN; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            BY SIMILA
ALPHA-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    HSSP, P02760; IBIK.
InterPro; IPR002223; Kunitz_BPTI.
InterPro; IPR00345; Lipocalin.
InterPro; IPR000566; Lipocalin.
Pfam; PF00014; Kunitz_BPTI; 2.
Pfam; PF00061; lipocalin; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CHAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL; U35642; AAB07599.1; -. PIR; A01209; TIBOBI.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           281
337
53
111
1111
137
149
188
281
264
277
337
333
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     149
91
                                                                                                                                                                                                                                          plasma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Lipocalin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CARBOHYD
CARBOHYD
CARBOHYD
CONFLICT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ACT_SITE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ACT SITE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         BINDING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            BINDING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         BINDING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CHAIN
```

```
1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "Identification and cloning of human placental bikunin, a novel serine protease inhibitor containing two Kunitz domains."; J. Biol. Chem. 272:12202-12208(1997).
                                                                                                                                                                                                                                                        86 KTTLQQEKPDFCFLEEDPGICRGYITRYFYNQQTKQCERFKYGGCLGNMNNFETLEECKN 145
                                                                                                                                                                                                           ------CNLPIVQGPCRSYIQLWAFDAVKGKCVRFSYGGCKGNGNKFYSEKECKE 335
                                                                                                                                                                                                                                                                                                                                                                                                                                SPT2_HUMAN STANDARD; PRT; 252 AA.
043291, 000571; O14895; Q969E0;
16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
15-UN-2002 (Rel. 41, Last annotation update)
Kunitr-type protease inhibitor 2 precursor (Hepatocyte growth factor activator inhibitor type 2) (HAI-2) (Placental bikunin).
                                                                                                                                                                                        CAFKADDGPCRAIMKRFFFNIFTRQCEEFIYGGCEGNQNRFESLEECKKMCTRDNANRII 85
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE-98010584; PubMed-9346890;
Kawaguchi T., Qin L., Shimomura T., Kondo J., Matsumoto K., Denda
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    YEQUENCE FROM N.A.
TISSUB-Pancreatic cancer;
MEDLINE-98094245; PubMed-9434156;
Mueller-PillackF, PubMed-9434156;
Mueller-PillackF, G, Gress T.M.;
Buechler M., Adler G, Gress T.M.;
Cloning of a new Kunitz-YPpe procease inhibitor with a putative transmembrane domain overexpressed in pancreatic cancer.";
Biochim. Biophys. Acta 1395:88-95(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Strausberg R.;
Submitted (AUG-2001) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: INHIBITOR OF HGF ACTIVATOR. ALSO INHIBITS PLASMIN,
PLASMA AND TISSUE KALLIRKEIN, AND FACTOR XIA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            "Purification and cloning of hepatocyte growth factor activator inhibitor type 2, a Kunitz-type serine protease inhibitor."; J. Biol. Chem. 272:27558-27564(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE-97277372; Pubmed-9115294;
Marlor C.W., Delaria K.A., Davis G., Muller D.K., Greve J.M.,
                                                                                                                            DB 1; Length 352;
A -> D (IN REF. 4).
G -> L (IN REF. 2 AND 3).
E -> Q (IN REF. 2 AND 3).
SY -> AF (IN REF. 2 AND 3).
E -> Q (IN REF. 2 AND 3).
E -> R (IN REF. 2 AND 3).
W, ED31C5CA02E70B19 CRC64;
                                                                                                                                           Pred. No. 3.1e-15;
                                                                                                                                                          13; Mismatches
                                                                                                                            25.8%; Score 233.5; 37.7%; Pred. No. 3.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A., AND SEQUENCE OF 28-74.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A., AND VARIANT LEU-200.
                                                                                             39235 MW;
                                                                                                                                                            46; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TISSUE=Colon, and Ovary;
               268
274
299
330
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (Human)
217
268
274
298
330
346
352 AA;
                                                                                                                                           Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TISSUE-Placenta;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Tamburini P.P.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Kitamura N.
                                                                                                                                                                                                                                                                                                                      146 IC 147
                                                                                                                                                                                                                                                                                                                                                    336 YC 337
                                             CONFLICT
CONFLICT
CONFLICT
SEQUENCE
CONFLICT
                                                                                                                            Query Match
                                 CONFLICT
                                                                                                                                              Local
                                                                                                                                                                                                                                                                                                                                                                                                                       SPT2_HUMAN
                                                                                                                                                            Matches
                                                                                                                                                                                          56
                                                                                                                                                                                                                                                                                        287
                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 10
                                                                                                                                                                                                                                                                                        g
                                                                                                                                                                                                                                                                                                                                                  Dp
                                                                                                                                                                                                                                                                                                                                                                                                                                                  SPEFF
                                                                                                                                                                                                                        g
                                                                                                                                                                                                                                                        òγ
                                                                                                                                                                                                                                                                                                                        ŏ
```

-!- SUBCELLULAR LOCATION: Type I membrane protein (Potential).

```
This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               3,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           80 NANRIIKTT-------LQQEKPD------FCFLEEDPGICRGYITRYFYNQ 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  34 IHDFCLVSKVVGRCRASMPRWWYNVTDGSCQLFVYGGCDGNSNNYLTKEECLKKCATVTE 93
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          22 MHSFCAFKADDGPCRAIMKRFFFNIFTRQCEEFIYGGCEGNQNRFESLEECKKMC--TRD 79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
REACTIVE BOND (BY SIMILARITY).
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
N-LINKED (GLONAC. ..) (POTENTIAL).
V -> L.
VFIIGEVAR_012482.
-i- TISSUE SPECIFICITY: EXPRESSED IN PLACENTA, KIDNEY, PANCREAS, PROSTATE, TESTIS, THYMUS, AND TRACHEA.
-i- DOMAIN: THIS INHIBITOR CONTAINS TWO INHIBITORY DOMAINS.
-i- SIMILARITY: CONTAINS 2 BPTI/KUNITZ INHIBITOR DOMAINS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 24;
                                                                                                                                                                                                                                                                                                                       PRINTS; PR00759; BASILTANSE.
PRODOM; PR000222; Kunitz_BPT1; 2.
SMART; SM00131; KU; 2.
PR0STIE; PS00280; BPT1_KUNITZ_1; 2.
PROSTIE; PS00209; BPT1_KUNITZ_2; 2.
Serine procease inhibitor; Repeat; Glycoprotein; Transmembrane;
                                                                                                                                                                                                                                                                                                                                                                                                                                  KUNITZ-TYPE PROTEASE INHIBITOR 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 232; DB 1; Length 252;
Pred. No. 3e-15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               56; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           3 Q -> H (IN REF. 3).

11 R -> P (IN REF. 1).

53 R -> K (IN REF. 3).

28228 MW; A7D3360C0ECAB2B CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                               EXTRACELLULAR (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CYTOPLASMIC (POTENTIAL).
BPTI/KUNITZ INHIBITOR 1.
BPTI/KUNITZ INHIBITOR 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 24; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           118 QTKQCERFKYGGCLGNMNNFETLEECKNIC 147
                                                                                                                                                                                                                                                                                                      InterPro; IPR002223; Kunitz_BPTI.
Pfam; PF00014; Kunitz_BPTI; 2.
                                                                                                                                                                          EMBL, U78095; AAC02781.1; -- SEMBL, BC072705; AAB84031.1; -- EMBL, BC001669; AAH01568.1; -- EMBL, BC01705; AAH07705.1; -- EMBL, BC011955; AAH11955.1; -- EMBL, BC0112868; AAH11955.1; -- EMBL, BC012868; AAH12868.1; --
                                                                                                                                                               EMBL; AB006534; BAA25024.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      25.68;
                                                                                                                                                                                                                                                                              Genew; HGNC:11247; SPINT2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 46; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                  252
1197
218
252
88
183
71
71
84
84
84
1183
1166
179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                144
57
94
200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                252 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    63
48
1133
1142
1142
1143
57
57
200
                                                                                                                                                                                                                                                                                           605124;
                                                                                                                                                                                                                                                                 HSSP; P05067
                                                                                                                                                                                                                                                                                                                                                                                                                                            DOMAIN
TRANSMEM
DOMAIN
DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CONFLICT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DOMAIN
DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ACT_SITE
DISULFID
DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ACT_SITE
CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CONFLICT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CONFLICT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     VARIANT
                                                                                                                                                                                                                                                                                                                                                                                                                        SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                   CHAIN
                                                                                                                                                                                                                                                                                           MIM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Matches
  qq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            δλ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ğ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             δ
```

Mon Dec

3,

```
This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation—the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                    SPT2_MOUSE STANDARD; PRT; 252 AA.
09WU03; 09WU04; 09WU05;
16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Created
                                                                                                                                                                                                                                                                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               REACTIVE BOND (BY SIMILARITY).
N-LINKED (GLCNAC. . .) (POTENTIAL).
N-LINKED (GLCNAC. . .) (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SMART; SMO0131; KU; 2.
SMART; SMO0131; KU; 2.
SMART; SMO0131; KU; 2.
PROSITE; PS50279; BPTL KUNITZ_1; 2.
Serine protease inhibitor; Repeat; Glycoprotein; Transmembrane; Stgnal; Alternative splicing.

POTENTIAL.

RUNITZ-TYPE PROTEASE INHIBITOR 2.
KUNITZ-TYPE PROTEASE INHIBITOR 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ISOFOEM 1.
-1- DOMAIN: THIS INHIBITOR CONTAINS TWO INHIBITORY DOMAINS.
-1- SIMILARITY: CONTAINS 2 BPTI/KUNITZ INHIBITOR DOMAINS.
-1- THIS INHIBITORY DOMAINS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             REACTIVE BOND (BY SIMILARITY). BY SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CYTOPLASMIC (POTENTIAL).
BPTI/KUNITZ INHIBITOR 1.
BPTI/KUNITZ INHIBITOR 2.
                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A., AND ALTERNATIVE SPLICING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               BY SIMILARITY.
BY SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      POTENTIAL
                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE=99160423; PubMed=10049781;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Pfam; PF00014; Kunitz_BPT1; 2. PRINTS; PR00759; BASICPTASE. ProDom; PD000222; Kunitz_BPT1; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MGD; MGI:1338031; Spint2.
InterPro; IPR002223; Kunitz_BPTI.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL, AF099016; AAD22172.1; -. EBMEL, AF099019; AAD22173.1; -. EMBL, AF099020; AAD22174.1; -. HSSP; P05067; ICA0.
                                                                                                                                                                                                                                                                                                                             NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                            STRAIN=BALB/C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DOMAIN
TRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ACT_SITE
CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ACT_SITE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DOMAIN
RESULT 11
```

```
Yamamoto T., Yamamoto M., Sinohara H.;

Tinter-alpha-trypsin inhibitor and its related proteins in Syrian hamster urine and plasma.";

J. Biochem. 120:145-152(1996).

-!- FUNCTION: ALPHA-1-MCROGLOBULIN OCCURS IN MANY PHYSIOLOGICAL FUNDING PLASMA, URINE, AND CEREBROSPINAL FUID. IT APPEARS NOT ONLY AS A FREE MONOMER BUT ALSO IN COMPLEXES WITH IGA AND ALBUMIN (BY SIMILARITY).

-!- FUNCTION: INTER-ALPHA-TRYPSIN INHIBITOR, PRESENT IN PLASMA AND URINE, INHIBITS TRYPSIN, PLASMIN, AND LYSOSOMAL GRANULOCYTIC ELASTASE (BY SIMILARITY).

-!- FUNCTION: Trypstatin is a trypsin inhibitor. It inhibits blood coagulation factor Xa and tryptase about 100-fold more rapidly than portine pancreatic trypsin and chymase. It is a monomer but is also found in mast cells as a complex with tryptase (By
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AMBP_MESAU STANDARD; PRT; 349 AA.

060559; Q60558; Q9QW86; Q9QW87;
01-NOV-1997 (Rel. 35, created)
01-NOV-1997 (Rel. 35, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
15-JUN-2012 (Rel. 41, Last annotation update)
trypsin inhibitor light chain (ITI-LC) (Bikunin) (HI-30); Trypstatin].

AMBP POR ITIL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SUBUNIT: I'ALPHA-I plasma protease inhibitors are assembled from one or two heavy chains (H1, H2 or H3) and one light chain, bikunin. Inter-alpha-inhibitor (I-ALPHA-I) is composed of H1, H2 and bikunin, inter-alpha-like inhibitor (I-ALPHA-LI) of H2 and bikunin, and pre-alpha-inhibitor (P-ALPHA-I) of H3 and bikunin (By
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE-95110820; PubMed-7529051;
Ide H., Itch H., Nava Y.;
'Sequencing of cDNAs encoding alpha 1-microglobulin/bikunin of
Mongolian gerbil and Syrian golden hamster in comparison with man and
                                                                                                                                                                                                                                                                                77 -TRDNANR------IIKTTLQQEKPD------FCFLEEDPGICRGYITRYFYNQ 117
                                                                                                                                                                                                                                                                                                                      94 NTTDDMARNRNGADSSVLSVPRKQSAEDLSAEIFNYEEYCVPKAVTGPCRAAFPRWYYDT 153
                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                 22 MHSFCAFKADDGPCRAIMKRFFFNIFTRQCEEFIYGGCEGNQNRFESLEECKKMC---- 76
MISSING (IN ISOFORM 2 AND ISOFORM 3). PRKQSAEDLSAEIFN -> CFVELSVAALFLFYA (IN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Cricetinae;
                                                                                                                    25.5%; Score 231; DB 1; Length 252; 31.3%; Pred. No. 3.8e-15;
                                                                                                                                                          57; Indels
                                                                               B2FF4B86924D4F8F CRC64;
                                               ISUFURM 3).
MISSING (IN ISOFORM 3)
                                                                                                                                                            22; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       other species.";
Biochim. Biophys. Acta 1209:286-292(1994).
                                                                                                                                                                                                                                                                                                                                                                118 QTKQCERFKYGGCLGNMNNFETLEECKNIC 147
                                                                                                                                                                                                                                                                                                                                                                                       ISOFORM 3)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mesocricetus auratus (Golden hamster).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE OF 205-348, AND SUBUNITS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TISSUE-Plasma, and Urine;
MEDLINE-97018241; PubMed-8864857;
                                                                               27914 MW;
                                                                                                                                                            47; Conservative
                                                        129 :
252 AA;
                                                                                                                                       Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NCBI_TaxID=10036;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                similarity).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               similarity).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TISSUE-Liver;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mesocricetus
  VARSPLIC
VARSPLIC
                                                            VARSPLIC
                                                                               SEQUENCE
                                                                                                                      Ouerv Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AMBP_MESAU
                                                                                                                                                              Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FT
FT
FT
SQ
                                                                                                                                                                                                                                                                                   δ
                                                                                                                                                                                                                                                                                                                        g
                                                                                                                                                                                                                                                                                                                                                                QΥ
```

```
EECKKMCTRDNANRIIKTTLQQEKPDFCFLEEDPGICRGYITRYFYNQQTKQCERFKYGG
                                                                                                                                                                                                                  337 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Biochim. Biophys. Acta 1088:47-56(1991).
                                                                            130 CLGNMNNFETLEECKNICEDGPNGFQ 155
                                                                                                   MEDLINE=91113729; PubMed=1703444;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1-microglobulin and bikunin.";
FEBS Lett. 269:32-36(1990).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE OF 2-337 FROM N.A.
                                                                                                                                                                                                                    STANDARD;
                                       274 KECLOTCRTVAA----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      similarity).
                                                                                                                                                                                                                                                                                                                                                                                                                                                         NCBI_TaxID=9823;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AND ALBUMIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TISSUE-Liver;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         inhibitors.";
                                                                                                                                                                                                                                                                                                                                                                               AMBP OR ITIL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ELASTASE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Favakkol A.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    plasma
                                                                                                                                                                                                                                                                                                                                                            (Fragment)
70
                                                                                                                                                                               RESULT 13
                                   g
                                                                              ò
                                                                                                                                                                                                                                                                        This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         3;
                                                                                                                 yellow chromophore (By similarity).
PTM: Heavy chains are interlinked with bikunin via a chondroitin
4-sulfate bridge to the their C-terminal aspartate (By
                                                     PTM: The precursor is proteolytically processed into separately functioning proteins.

PTM: Alpha-1-microglobulin contains a covalently linked brown-
                                                                                                                                                                                               SIMILARITY: IN THE N-TERMINAL SECTION; BELONGS TO THE LIPOCALIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CHROMOPHORE (BY SIMILARITY).
CHROMOPHORE (BY SIMILARITY).
BY SIMILARITY.
N-LINKED (GLCNAC. .) (POTENTIAL).
N-LINKED (GLCNAC. .) (POTENTIAL).
SUBCELLULAR LOCATION: Secreted. TISSUE SPECIFICITY: Synthesized in the liver and secreted in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 INTER-ALPHA-TRYPSIN INHIBITOR LIGHT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           N-LINKED (GLCNAC. . .) (POTENTIAL).
INHIBITORY SITE (P1) (CHYMOTRYPSIN,
ELASTASE) (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Glycoprotein; Plasma; Signal; Serine protease inhibitor; Repeat;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             INHIBITORY SITE (P1) (TRYPSIN) (BY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                24.6%; Score 223; DB 1; Length 349; 32.2%; Pred. No. 3.1e-14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       BPTI/KUNITZ INHIBITOR 1.
BPTI/KUNITZ INHIBITOR 2.
CHROMOPHORE (BY SIMILARITY).
                                                                                                                                                                                                                                       SIMILARITY: CONTAINS 2 BPTI/KUNITZ INHIBITOR DOMAINS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SIMILARITY)
SIMILARITY)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -> E (IN REF. 2).
8C954584B7DBE728 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ALPHA-1-MICROGLOBULIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             55;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (BY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       24; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SIMILARITY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CHROMOPHORE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TRYPSTATIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     InterPro; IPR00223; Kunitz_BPTI.
InterPro; IPR002345; Lipocalin.
InterPro; IPR000366; Lipocalin.
Pfam: PF00014; Kunitz_BPTI; 2.
Pfam: PF00061; lipocalin; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PROSITE; PS00280; BPTI_KUNITZ_1; 2. PROSITE; PS50279; BPTI_KUNITZ_2; 2. PROSITE; PS00213; LIPOCALIN; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRINTS; PRO0759; BASICPTASE.
PRINTS; PRO0179; LIPOCALIN.
PRODOM; PD000222; Kunitz_BPTI; 2.
SWART; SW00131; KU; E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      342 342 G
349 AA; 38782 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL; D31814; BAA06601.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              52
1110
1136
1148
1148
1187
2280
263
                                                                                                                                                                                                                                                                                                                                                                                                                                                             P02760; 1BIK.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Local Similarity
                                                                                                                                                                               similarity).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      282
230
286
286
52
110
110
136
90
230
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 296
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       47;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Lipocalin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        BINDING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ACT_SITE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ACT_SITE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CONFLICT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DOMAIN
BINDING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   BINDING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         BINDING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Best Loca
Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CHAIN
  1 .
                                                                                                                                                                                                 <u>-</u>-
                                                                                                                                                                                                                                       <u>-</u>-
```

10 IITDTELPPLKLMHSFCAFKADDGPCRAIMKRFFFNIFTRQCEFFIYGGCEGNQNRFESL 69

ò

```
SUBDIVIT: I-ALPHA-I plasma protease inhibitors are assembled from one or two heavy chains (H1, H2 or H3) and one light chain, blundin. Inter-alpha-inhibitor (I-ALPHA-I) is composed of H1, H2 and blkunin, inter-alpha-like inhibitor (I-ALPHA-I) of H2 and blkunin, and pre-alpha-inhibitor (P-ALPHA-I) of H3 and blkunin (BY
                                                                                                                                                                                                                     P04366; P34954;
20-MAR-1987 (Rel. 04, Created)
01-FBE-1994 (Rel. 28, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
AMBP protein precursor (Contains: Alpha-1-microglobulin; Inter-alpha-trypsin inhibitor light chain (ITI-LC) (Bikunin) (HI-30) (EI-14)]
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               "Molecular cloning of porcine alpha 1-microglobulin/HI-30 reveals developmental and tissue-specific expression of two variant messenger ribonucleic acids.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE OF 212-334.
MEDLINE-8522567; PubMed-2408637;
Hochstrasser K., Wachter E., Albrecht G.J., Reisinger P.;
"Kunitz-type proteinase inhibitors derived by limited proteolysis of the inter-alpha-trypsin inhibitor, X. The amino-acid sequences of the trypsin-released inhibitors from horse and pig inter-alpha-trypsin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPEARS NOT ONLY AS A FREE MONOMER BUT ALSO IN COMPLEXES WITH IGA
MEDLINE=90353595; PubMed=1696914; Gebhard W., Schreitmueller T., Vetr H., Wachter E., Hochstrasser K.; "Complementary DNA and deduced amino acid sequences of procine alpha
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           separately functioning proteins.
PTM: Alpha-L-microglobulin contains covalently linked brown-ptM: Alpha-L-microglobulin contains covalently linked brown-syallow chromophores (By similarity).
SIMILARITY: IN THE N-TERMINAL SECTION; BELONGS TO THE LIPOCALIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FUNCTION: INTER-ALPHA-TRYPSIN INHIBITOR, PRESENT IN PLASMA AND URINE, INHIBITS TRYPSIN, PLASMIN, AND LYSOSOMAL GRANULOCYTIC
                                                                                                                                                                                                                                                                                                                                                                                   Sus scrofa (Pig).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Cetartiodactyla, Suina, Suidae, Sus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Biol. Chem. Hoppe-Seyler 366:473-478(1985).
-!- FUNCTION: ALPHA-1-MICROGLOBULIN OCCURS IN MANY PHYSIOLOGICAL
FLUIDS INCLUDING PLASMA, URINE, AND CEREBROSPINAL FLUID. IT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SUBCELLUIAR LOCATION: Secreted.
TISSUE SPECIFICITY: Synthesized in the liver and secreted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PTM: The precursor is proteolytically processed into two
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FAMILY. SIMILARITY: CONTAINS 2 BPTI/KUNITZ INHIBITOR DOMAINS.
```

```
This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              86 KTTLQQEKPDFCFLEEDPGICRGYITRYFYNQQTKQCERFKYGGCLGNMNNFETLEECKN 145
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          272 ------CSLPIVSGPCRGFFQLWAFDAVQGKCVLFNYGGCQGNGNQFYSEKECKE 320
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  216 COLGYSQGPCLGMIKRYFYNGSSMACETFHYGGCMGNGNNFVSEKECLQTCRTVEA--- 271
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        26 CAFKADDGPCRAIMKRFFFNIFTRQCEEFIYGGCEGNQNRFESLEECKKMCTRDNANRII 85
                                                                                                                                                                                                                                        PROSITE; PS00280, BPTI_KUNITZ_1; 2.
PROSITE; PS00280, BPTI_KUNITZ_1; 2.
PROSITE; PS00213; LIPOCALIN; 1.
Glycoprotein; Plasma; Signal; Serine protease inhibitor; Repeat;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                N-LINKED (GLCNAC. . .) (POTENTIAL).
N-LINKED (GLCNAC. . .).
                                                                                                                                                                                                                                                                                                                                                                         INTER-ALPHA-TRYPSIN INHIBITOR LIGHT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           INHIBITORY SITE (P1) (CHYMOTRYPSIN,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ELASTASE).

INHIBITORY SITE (P1) (TRYPSIN).

I > M (IN REF. 2).

E >> Q (IN REF. 3).

E >> Q (IN REF. 3).

E >> Q (IN REF. 3).

C >> A (IN REF. 3).

C >> A (IN REF. 3).

C >> A (IN REF. 3).

V >> A (IN REF. 3).

C >> X (IN REF. 3).

E >> Q (IN REF. 3).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      24.4%; Score 220.5; DB 1; Length 337;
                                                                                                                                                                                                                                                                                                                                                                                                 BPII/KUNITZ INHIBITOR 1.
BPII/KUNITZ INHIBITOR 2.
CHROMOPHORE (BY SIMILARITY).
CHROMOPHORE (BY SIMILARITY).
CHROMOPHORE (BY SIMILARITY).
CHROMOPHORE (BY SIMILARITY).
BY SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1F630FF98E3CD70F CRC64;
                                                                                                                                                                                                                                                                                                                                                           ALPHA-1-MICROGLOBULIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                49:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; Pred. No. 5.1e-14; 14; Mismatches 49
                                                                                                                                                                                                                                                                                                                                              SIMILARITY
                                                                                                                                                                            InterPro; IPR002223; Kunitz_BPTI.
InterPro; IPR000566; Lipocln_cytFABP.
Pfam; PF00014; Kunitz_BPTI; 2.
Prodom; PD000222; Kunitz_BPTI; 2.
SMART; SM00131; KU; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          37690 MW;
                                                                                                            EMBL; X53685; CAA37725.1; -. EMBL; X52087; CAA36306.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
                                                                                                                                                                                                                                                                                                                                              4
188
337
                                                                                                                                      PIR; A01208; TIPGBI.
PIR; S11066; S11066.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             311
315
337 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Local Similarity
nes 44; Conserv
                                                                                                                                                      PIR; S11066; S11060
HSSP; P02760; 1BIK
                                                                                                                                                                                                                                                                                                                                1
4
191
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              YC 322
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     146 IC 147
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DISULFID
DISULFID
DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CONFLICT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ACT_SITE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE
                                                                                                                                                                                                                                                                                                                                  NON_TER
SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ACT_SITE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CONFLICT
                                                                                                                                                                                                                                                                                                                                                                                                                DOMAIN
BINDING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CONFLICT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CONFLICT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CONFLICT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CONFLICT
                                                                                                                                                                                                                                                                                                                                                                                                                                            BINDING
                                                                                                                                                                                                                                                                                                                                                                                                                                                         BINDING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      BINDING
                                                                                                                                                                                                                                                                                                                                                                                                 DOMAIN
                                                                                                                                                                                                                                                                                                                                                            CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              321
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Best Loc
Matches
  ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     δ
```

```
This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STRAIN—C57BL/6; TISSUB-Liver;

A Itoh H., Ide H., Yoshihara H., Nawa Y.;

L. Submitted (JAN-1994) to the EMBL/GenBank/DDBJ databases.

L. Submitted (JAN-1994) to the EMBL/GenBank/DDBJ databases.

PLUIDS INCLUDING PLASMA, URINE, AND CEREBROSPINAL FLUID. IT

APPEARS NOT OUL AS A FREE MONOMER BUT ALSO IN COMPLEXES WITH IGA

AND ALBUMIN (BY SIMILARITY).

-I- FUNCTION: INTER-ALPHA-TRYPSIN INHIBITOR, PRESENT IN PLASMA AND

C ILLASTASE (BY SIMILARITY).

-I- SUBUNIT: I-ALPHA-I plasma protease inhibitors are assembled from

One or two heavy chains (H., H2 or H3) and one light chain,

bikunin. Inter-alpha-inhibitor (I-ALPHA-I) is composed of H1, H2

and bikunin, inter-alpha-inhibitor (I-ALPHA-II) of H2 and

bikunin, and pre-alpha-inhibitor (P-ALPHA-II) of H3 and bikunin (By
                                                                                                                                                                                                                                                                                                                                                                                         Chan P., Salier J.P.; "Mouse alpha-1-microglobulin/bikunin precursor: cDNA analysis, gene evolution and physical assignment of the gene next to the orosomucoid
                                         007456; 061294;
01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 41, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
AMBP protein precursor [Contains: Alpha-1-microglobulin; Inter-alpha-trypsin inhibitor light chain (ITI-LC) (Bikunin) (HI-30)].
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
STRAIM-CSTBL-16. TISSUE-Liver;
STRAIM-CSTBL-6; TISSUE-Liver;
STRAIM-CSTBL-74: PubMed=7533761;
Itch H., Ide H., Kataoka H., Tomita M., Yoshihara H., Nawa Y.;
Toh M., Ide H., Rataoka H., Tomita M., Yoshihara H., Nawa Y.;
Toh M., Sequencing of mouse alpha 1-microglobulin/Inter-alpha-trypsin inhibitor light chain and its expression in acute inflammation.";
J. Blochem. 116:767-772(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               separately functioning proteins.
--- PTM: Alphal-Imicroglobulin contains covalently linked brown-yellow chromophores (By similarity).
--- SIMILARITY: IN THE N-TERMINAL SECTION; BELONGS TO THE LIPOCALIN
                                                                                                                                                                                                        Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -1- TISSUE SPECIFICITY: Synthesized in the liver and secreted in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -!- PTM: The precursor is proteolytically processed into two
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -!- SIMILARITY: CONTAINS 2 BPTI/KUNITZ INHIBITOR DOMAINS
                          349 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Biochim. Biophys. Acta 1174:195-200(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                similarity). Subcellular Localion: Secreted.
                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
STRAIN-BALB/c; TISSUE-Liver;
MEDLINE-93363639; Pubmed-7689339;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE OF 128-349 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL; X68680; CAA48640.1; -.
EMBL; D28812; BAA05973.1; -.
HSSP; P02760; IBIK.
                          STANDARD;
                                                                                                                                                                                                                                                                              NCBI_TaxID=10090;
                                                                                                                                                                                       AMBP OR ITIL.
                          AMBP_MOUSE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ocus."
AMBP_MOUSE
```

```
GNONRFESLEECKKMCTRDNANRIIKTTLQQEKPDFCFLEEDPGICRGYITRYFYNQQTK 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                265 GNGNNFISEKDCLQTC-----RTIAA-----CNLPIVQGPCRAFIKLWAFDAAQG 309
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           20; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DSEEDEEHTIITDTELPPLKLMHSFCAFKADDGPCRAIMKRFFFNIFTRQCEEFIYGGCE 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-JAN-1990 (Rel. 13, Last Sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Inter-alpha-trypsin inhibitor (ITI) (GIK-14) (Inhibitory fragment of ITI) (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CHROMOPHORE (BY SIMILARITY).
BY SIMILARITY.
N-LINKED (GLCNAC. ..) (POTENTIAL).
N-LINKED (GLCNAC. ..) (POTENTIAL).
N-LINKED (GLCNAC. ..) (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Capra hircus (Goat).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    N-LINKED (GLCNAC. ..) (POTENTIAL).
N-LINKED (GLCNAC. ..) (POTENTIAL).
INHIBITORY SITE (P1) (CHYMOTRYPSIN,
ELASTASE) (BY SIMILARITY).
INHIBITORY SITE (P1) (TRYPSIN) (BY
                                                                                                                                                                                                                                                                                                                                                                                                                                                 ALPHA-1-MICROGLOBULIN.
INTER-ALPHA-TRYPSIN INHIBITOR LIGHT
                                                                                                                                                                                                                                                                                                                                                              Glycoprotein; Plasma; Signal; Serine protease inhibitor; Repeat;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  24.0%; Score 217; DB 1; Length 349; 32.9%; Pred. No. 1.2e-13; Live 23; Mismatches 61; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -> S (IN REF. 2).
CE4D9FC7375DA80B CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 BPTI/KUNITZ INHIBITOR 1. BPTI/KUNITZ INHIBITOR 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         121 QCERFKYGGCLGNMNNFETLEECKNICEDGPNGFQ 155
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         310 KCIQFHYGGCKGNGNKFYSEKECKEYCGVPGDGYE 344
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    123 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SIMILARITY)
                                                                                                                                                             PRINTS; PR00759; BASICPTASE.
PRINTS; PR00179; LIPOCALIN.
ProDom; PD000222; Kunitz_BPTI; 2.
SMART; SMO0131; KU; 2.
PROSITE; PS00280; BPTI_KUNITZ_1; 2.
PROSITE; PS00213; LIPOCALIN; 1.
MGD; MGI:88002; Ambp.
InterPro; IPR00223; Kunitz_BPTI.
InterPro; IPR002345; Lipocalin.
InterPro; IPR003565; Lipocalin.
Pfam; PF00014; Kunitz_BPTI, 2.
Pfam; PF00061; lipocalin; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-JAN-1990 (Rel. 13, Created)
01-JAN-1990 (Rel. 13, Last seq
16-OCT-2001 (Rel. 40, Last ann
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    39070 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           51; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Bovidae; Caprinae; Ovis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Ovis aries (Sheep), and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 349 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    296
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    IATR_SHEEP
                                                                                                                                                                                                                                                                                                                                                                                                Lipocalin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         BINDING
BINDING
DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ACT_SITE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ACT_SITE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DOMAIN
BINDING
BINDING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CONFLICT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                          SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                 CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   P1337
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AC DE DT DT OC OC OC OC OC
        DOR NO DO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ŏ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         δλ
```

```
Rasp G., Hochstrasser K., Gerl C., Wachter E.;

"Primary structure of a proteinase inhibitor released from goat serum inter-alpha-trypsin inhibitor.";

Biochim. Biophys. Acta 999-335-337(1989).

-!- FUNCTION: THIS INHIBITORY FRAGMENT, RELEASED FROM NATIVE ITI AFTER LIMITED PROTEOLYSIS WITH TRYPSIN, CONTAINS TWO HOWOLOGOUS DOMAINS. WHEREAS THE SECOND DOMAIN IS A STRONG INHIBITOR OF TRYPSIN, THE FIRST DOMAIN INTEREACH WEAKLY WITH PANN-CRANULOCYTIC ELASTASE AND NOT AT ALL WITH PANCREATIC ELASTASE.

-!- MISCELLANGOUS: THE AMINO ACID AT POSITION P2' (17) APPEARS TO DETERMINE THE SPECIFICITY OF THE INHIBITION OF DOMAIN I.

INHIBITORS WITH METHIONINE IN THIS POSITION INTERACT WEAKLY WITH CHYMOTRYPSIN AND ELASTASE: THOSE WITH LEUCINE INTERACT STRONGLY.
                                                                                                                                                                                                 Rasp G., Hochstrasser K., Wachter E., Reisinger P.W.M.; "The amino-acid sequence of the trypsin-released inhibitor from sheep inter-alpha-trypsin inhibitor."; Inter-alpha-trypsin inhibitor."; Biol. Chem. Hoppe-Seyler 368:727-731(1987).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  86 KTTLQQEKPDFCFLEEDPGICRGYITRYFYNQQTKQCERFKYGGCLGNMNNFETLEECKN 145
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             5 CQLGYSQGPCLGMFKRYFYNGTSMACETFYYGGCMGNGNNFPSEKECLQTC----- 55
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   26 CAFKADDGPCRAIMKRFFFNIFTRQCEEFIYGGCEGNQNRFESLEECKKMCTRDNANRII 85
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                BPTI/KUNITZ INHIBITOR 1.
BPTI/KUNITZ INHIBITOR 2.
BY SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 216.5; DB 1; Length 123; Pred. No. 4.4e-14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PIRSON STATEMENTS CONTAINS 2 BPTI/KUNITZ INHIBITOR DOMAINS.
PIRS, A29652. A29652.
HISSP, P02760; JBIK.
A16SP, P027
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             INHIBITORY SITE (P1) (TRYPSIN).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 48; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      13686 MW; 295038173F22D2D1 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    N-LINKED (GLCNAC. . .).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 13; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Search completed: December 2, 2002, 10:02:53 Job time: 18.0199 secs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ELASTASE)
                                                                                                                                                                                                                                                                                                                                                                                                                                                       SPECIES-C.hircus;
MEDLINE-90105540; PubMed-2481505;
                                                                                                                        SPECIES-Sheep;
MEDLINE=87299012; PubMed=2441725;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   23.98;
37.78;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         55
111
111
55
38
51
111
111
107
NCBI_TaxID=9940, 9925;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 123 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     146 IC 147
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       110 YC 111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     46;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NON_TER
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ACT_SITE
CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ACT_SITE
                                                                                      SEOUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    염
    NAME OF THE PETT O
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ŏ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ŏ
```

5

```
Compugen Ltd.
GenCore version 5.1.3
Copyright (c) 1993 - 2002 Compug
                                                                                                        OM protein - protein search, using sw model
```

December 2, 2002, 10:00:15; Search time 57.6716 Seconds (without alignments) 575.215 Million cell updates/sec Run on:

US-09-741-106-19 905

1 DSEEDEEHTIITDIELPPLK......ECKNICEDGPNGFQVDNYGT 161 Perfect score: Sequence:

Gapop 10.0 , Gapext 0.5 Scoring table:

Total number of hits satisfying chosen parameters:

671580 segs, 206047115 residues

Searched:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

SPIREMBL 21:\* Database :

sp\_virus:\*
sp\_vertebrate:\*
sp\_unclassified:\* sp\_invertebrate:\*
sp\_mammal:\*
sp\_mhc:\* sp\_rvirus:\*
sp\_bacteriap:\* sp\_archea:\*
sp\_bacteria:\*
sp\_fungi:\*
sp\_human:\* sp\_organelle:\* sp\_archeap:\* sp\_plant:\* sp\_rodent:\* sp\_phage:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# STIMMARTES

	Description	Q28874 canis famil	093424 cyprinus ca	Q8wpi2 boophilus m	Q8wpi3 boophilus m	Q9u8g8 manduca sex	076840 caenorhabdi	Q9n343 caenorhabdi	044938 haemonchus	O45881 caenorhabdi	Q9vav4 drosophila	Q27422 caenorhabdi	Q18761 caenorhabdi	Q99qr0 drosophila	Q21418 caenorhabdi	Q09983 caenorhabdi	062504 caenorhabdi
SUMMARIES	ID	Q28874	093424	Q8WPI2	Q8WPI3	0908G8	076840	Q9N343	044938	045881	Q9VAV4	027422	018761	Q9GQR0	Q21418	009983	062504
	DB	9	13	Ŋ	2	S	S	ഗ	Ŋ	Ŋ	വ	Ŋ	ហ	വ	വ	വ	Ŋ
	% puery fatch Length DB	396	287	142	142	3198	2167	1195	1572	2225	3060	838	838	2174	922	1599	1474
	% Query Match	60.8	40.0	34.5	33.3	29.7	29.4	28.6	28.5	28.5	28.1	27.8	27.8	27.4	27.0	26.6	26.0
	Score	550	362	312.5	301.5	268.5	266.5	258.5	258	257.5	254.5	252	252	248	244	240.5	235
	Result No.	1	7	E)	4	S	9	7	80	6	10	11	12	13	14	15	16

Q22685 caenorhabdi	045916 caenorhabdi	P70004 xenopus lae	Q9xwx5 caenorhabdi	O70160 cavia porce	Q9dbj9 mus musculu	Q925wl mus musculu	Q9d3k4 mus musculu	Q99j04 mus musculu	Q19021 caenorhabdi	O17644 caenorhabdi	P78491 homo sapien	O8teu8 homo sapien	Q964q0 ixodes scap	O16784 caenorhabdi	Q19305 caenorhabdi	Q9gqn2 calliactis	Q9gqnl calliactis	Q90w98 pseudonaja	Q9twg0 anemonia su	Q96nz8 homo sapien	Q23456 caenorhabdi	Q9n0x7 bos taurus	Q965ml caenorhabdi	О	Q91484 salmo salar	Q9tui0 sus scrofa	_	Q99k32 mus musculu
5 022685	5 045916	13 P70004	2	11	11	11	11	11	2	2	4	4	Ŋ	Ŋ	5 Q19305	S	S	13	S	4	ហ	9	S	9	13 Q91484	9	4	11 Q99K32
۲.	.0	9.	24.4 1743	0.	24.0 349										20.9 805			æ							18.7 372			
233	226.5	223	221	217.5	217	217	213.5	213.5	206.5	203	199.5	199	197.5	190.5	189.5	182	182	179	175	174.5	173.5	173	171.5	169.5	169.5	167.5	167	167
17	18	19	20	21	22	23	24	25	26	27	28	29	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45

### ALIGNMENTS

```
MEDLINE-95071310; PubMed-7980463; Girard T.J., Gailani D., Broze G.J.Tr.; Complementary DNA sequencing of canine tissue factor pathway inhibitor reveals a unique nanomeric repetitive sequence between the second and third Kunitz domains."; Blochem. J. 303:923-928(1994).

EMBL; S75369; AAB32443.1; -...
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      3 EEDEEHTIITDTELPPLKLMHSFCAFKADDGPCRAIMKRFFFNIFTRQCEEFIYGGCEGN 62
                                                                                                                                          Eukaryota; Metazoa, Chordata, Craniata; Vertebrata, Euteleostomi;
Mammalia; Eutheria, Carnivora; Fissipedia, Canidae; Canis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 396;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      21; Indels
                                                                                                                                                                                                                                                                                                                                                  nestre float.
Interpro; IRR00223; Kunitz_BPTI.
Pfam; PF00014; Kunitz_BPTI; 3.
PRINTS; PR00759; BASICPTASE.
ProDom; PD000222; Kunitz_BPTI; 3.
SMART; SM00131; KU; 3.
PROSITE; PS00280; BPTI KUNITZ_1; 3.
PROSITE; PS50279; BPTI_KUNITZ_2; 3.
Serine procease inhibitor.
Secuence 396 AA; 43948 MW; 50F65C8337A003D9 CRC64;
                                                         01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
11-MAR-2002 (TrEMBLrel. 20, Last annotation update)
Tissue actor pathway inhibitor.
Canis familiaris (Dog).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    60.8%; Score 550; DB 6; 65.8%; Pred. No. 1.3e-52; tive 24; Mismatches 21
                            396 AA
                              PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
                              PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Local Similarity
les 98; Conserv
                                                                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                          NCBI_TaxID=9615;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Matches
RESULT 1
                028874
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      QΩ
                                 δ
```

4;

```
Query Match
                                                                                                                                                                                   Signal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Q8WPI3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Signal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Q8WPI3
                                                                                                                                                                                                                                                                 Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                      28WPI3
ōλ
                                                                                                                                                                                                                                                                                                                                                          q
                                                                                                                                                                                                                                                                                                                                                                                 δλ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         δà
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ;;
        63 QNRFESLEECKKMCTRDNANRIIKT-TLQQ--EKPDFCFLEEDPGICRGYITRYFYNQQT 119
                     90 QNRFESLEECEEKCVRVYPK--AKTETLEKVLEKPDYCHMNEDSGLCRGFVTRYYYNNVS 147
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  79 DNANRIIKTTLQQEKPDFCFLEEDPGICRGYITRYFYNQQTKQCERFKYGGCLGNMNNFE 138
                                                                                                                                                      01-NOV-1998 (TrEMBLrel. 08, Created)
01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
01-NAR-2002 (TrEMBLrel. 20, Last annotation update)
Hypothetical 33.1 Kba protein.
Cyprinus carpio (Common carp).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        19 LKLMHSFCAFKADDGPCRAIMKRFFFNIFTRQCEEFIYGGCEGNQNRFESLEECKKMCTR 78
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A. Prasa D., Stuerzebecher J., Sures I., Friedrich T., Pereira P.J., Prasa D., Stuerzebecher J., Sures I., Friedrich T.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Boophilin precursor. (Cattle tick).
Boophilus microplus (Cattle tick).
Eukaryota; Metazoa; Arthropoda; Chelicerata; Arachnida; Acari;
Parasitiformes; Ixodida; Ixodidae; Boophilus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                           40.0%; Score 362; DB 13; Length 287;
43.8%; Pred. No. 5.9e-32;
ive 29; Mismatches 36; Indels 12
                                                                                                                                                                                                                                                                                               Gracey A.Y.;
Submitted (JUN-1998) to the EMBL/GenBank/DDBJ databases.
EMBL, AF008648; AAC19410.1; -.
HSSP; P31713; 1SHP.
                                                                                                                                                                                                                                                                                                                                                                                                   PROSITE; PS00280; BPTI_KUNITZ_1; 3.
PROSITE; PS50279; BPTI_KUNITZ_2; 3.
HYPOTHELICAL protein; Serine protease inhibitor.
SEQUENCE 287 AA; 33093 MW; DF6983D76718115E CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-MAR-2002 (TrEMBLrel. 20, Created)
01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Pereira P.J., Prasa D., Stuerzebecher J., Sures J
Mentele R., Huber R., Bode W., Fuentes-Prior P.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   142 AA.
                                                    120 KQCERFKYGGCLGNMNNFETLEECKNICE 148
                                                                 PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRT;
                                                                                                                                                                                                                                                                                                                                        Interpro; IPR002233; Kunitz_BPTI.
Pfam; PF00014; Kunitz_BPTI; 3.
PRINTS; PR00759; BASICPTASE.
ProDom; PD000222; Kunitz_BPTI; 3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   139 TLEECKNICEDGPNGFQ 155
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          143 TIKECHERCLPALNNME 159
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Best Local Similarity 43.8 Matches 60; Conservative
                                                                                                                                    PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                          SMART; SM00131; KU; 3.
                                                                                                                                                                                                                                      Cyprinidae; Cyprinus.
NCBI_TaxID=7962;
                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
TISSUE=LIVER;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NCBI_TaxID=6941;
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Q8WPI2
Q8WPI2;
                                                                                                                                   093424
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            6
                                                                                                              RESULT 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 3
                                                                                                                       Q8WPI2
                                                                         g
                            염
                                                      õ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     δλ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ద
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ò
```

```
82 NRIIKTTLQQEKPDF---CFLEEDPGICRGYITRYFYNQQTKQCERFKYGGCLGNMNNFE 138
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
"Boophilin is a novel Kunitz-type thrombin inhibitorIsolation, characterization, cloning and three-dimensional model of its complex
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mentele R., Huber R., Bode W., Fuentes-Prior P., "Boophilin is a novel Kunitz-type thrombin inhibitorisolation, characterization, cloning and three-dimensional model of its complex
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              23 HSFCAFKADDGPCRAIMKRFFFNIFTRQCEEFIYGGCEGNQNRFESLEECKKMC-TRDNA 81
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Pereira P.J., Prasa D., Stuerzebecher J., Sures I., Friedrich T.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Boophilin precursor.

Boophilus microplus (Cattle tick).

Bushivota, Metazoa; Arthropoda; Chelicerata; Arachnida; Acari;

Barasitiformes; Ixodida: Ixodidae: Boophilus.

NCBL_TaxID=6941;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  34.5%; Score 312.5; DB 5; Length 142; 44.3%; Pred. No. 8.4e-27; Live 22; Mismatches 40; Indels 11;
                                                                                              Submitted (DEC-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                         Pereira P.J.;
Thesis (1999), Universidade do Porto, Oporto, Portugal.
EMBL: AJ304447; CAC82583.1; -.
InterPro; IPR002223; Kunitz_BPTI.
Pfam; PF00014; Kunitz_BPTI. 2.
PRINTS; PR000759; BASICPTASE.
ProDom; PD000222; Kunitz_BPTI; 2.
PROSITE; SM00131; KU; 2.
PROSITE; PS50279; BPTI KUNITZ_1; UNKNOWN_2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Submitted (DEC-2000) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Pereira P.J.;
Thesis (1999), Universidade do Porto, Oporto, Portugal.
EMBL: AJ304446; CAC82582.1; -.
InterPro; IPR002223; Kunitz_BPTI.
Pfam; PR00014; Kunitz_BPTI.
PRODOM; PR000759; BASICEPRASE.
ProDom; PR00759; BASICEPRASE.
PRODOM; SM00131; KU; Z.
PROSITE; PS00280; BPTI.KUNITZ_1; UNKNOWN_2.
PROSITE; PS50279; BPTI.KUNITZ_1; UNKNOWN_2.

        SIGNAL
        1
        15
        POTENTIAL.

        CHAIN
        16
        142
        BOOPHILIN, ISOFORM H2.

        SEQUENCE
        142 AA; 15538 MW; 88BF0008BBD42010 CRC64;

                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            BOOPHILIN, ISOFORM G2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-MAR-2002 (TrEMBLrel. 20, Created)
01-MAR-2002 (TrEMBLrel. 20, Last sequ
01-JUN-2002 (TrEMBLrel. 21, Last anno
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Local Similarity 44.3%
es 58; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   139 TLEECKNICED 149
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          131 SEEECELVCKN 141
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      16
                                                                    withthrombin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             withthrombin
```

3;

```
076840; Q22911;
01-NOV-1998 (TrEMBLrel. 08,
01-NOV-1998 (TrEMBLrel. 08,
01-MAR-2002 (TrEMBLrel. 20,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           52; Conservative
                                                                                                                                                PRELIMINARY;
                                                                                                                                                                                                                                     Caenorhabditis elegans.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  77 ----TRDNANR-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Local Similarity
                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                            STRAIN-BRISTOL N2;
                                                                                                                                                                                                            C37C3.6 protein.
C37C3.6.
                                                                                                                                                                                                                                                                                                                                                                                       OF FORM B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                VARSPLIC
VARSPLIC
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
                                                                                                                                                076840
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Matches
                                                                                                                       RESULT 6
076840
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Dp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           qq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           q
                                                                                                                                                              ŏλ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     δλ
                                   Д
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   δλ
                                                             δλ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         3
                                                5
                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE-99457716; PubMed-10528409; Nardi J.B., Robertson H.M.; Nardi J.B., Martos R., Walden K.K., Lampe D.J., Robertson H.M.; Expression of lacunin, a large multidomain extracellular matrix protein, accompanies morphogenesis of epithelial monolayers in Manduca
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2376 DSGDSCRHTGVFPIQEACERTCGAFRNINVCRYDLDPGPCRTYEAKYFFDKASRSCREFA 2435
                                                                                                                                    83 RIIKTTLQQEKPDF---CFLEEDPGICRGYITRYFYNQQTKQCERFKYGGCLGNMNNFET 139
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        19; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 DSEEDEEHTIITDTELPPLKLMHSF-----CAFKADDGPCRAIMKRFFFNIFTRQCEEFI 55
                                                                                     Manduca sexta (Tobacco hawkmoth) (Tobacco hornworm).
Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Petryqota; Neoptera; Endopteryqota; Lepidoptera; Glossata; Ditrysia;
Sphingiodea; Sphingidae; Sphinginae; Manduca.
                                                                        23 HSFCAFKADDGPCRAIMKRFFFNIFTRQCEEFIYGGCEGNQNRFESLEECKKMCTRDNAN 82
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 3198;
                       33.3%; Score 301.5; DB 5; Length 142; 42.3%; Pred. No. 1.4e-25;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Immunoglobulin domain; Serine protease inhibitor; Signal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE 3198 AA; 349364 MW; AB4ACD459C0D9134 CRC64;
142 AA; 15555 MW; EA6EC742D3599705 CRC64;
                                                                                                                                                                                                                                                                                  01-WAY-2000 (TrEMBLrel. 13, Created)
01-WAY-2000 (TrEMBLrel. 13, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 268.5; DB 5 Pred. No. 1.7e-20;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          sexta.";
Insect Blochem. Mol. Biol. 29:883-897(1999).
EMBL; AF078161; AAR04457.1;
HSSP; P12111; ZKNT.
InterPro; IPR004094; Antistasin.
InterPro; IPR003598: 19_C2.
InterPro; IPR003223; Kunitz_BPTI.
InterPro; IPR0002223; Kunitz_BPTI.
InterPro; IPR000884; TSPI.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     29.7%: Scor.
33.3%; Pred. No. 1...
've 25; Mismatches
                                                24; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Pfam, FF00014; Mallian, FF00014; PRINTS, PF00014; PRONO529; PASTCPTASE.
PLODOM; P0000222; Kunitz_BPT1; 10.
SMART; SM00131; KU; 10.
SMART; SM00131; KU; 10.
SMART; SM00131; KU; 10.
SMART; SM00131; YSP1; 7.
PROSITE; PS00317; WAP; 1.
PROSITE; PS00317; WAP; 1.
PROSITE; PS00209; BPTL_KUNITZ_1; 8.
PROSITE; PS500279; BPTL_KUNITZ_2; 10.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Pfam; PF02822; Antistasin; 4.
Pfam; PF00047; ig; 2.
Pfam; PF00014; Kunitz_BPTI; 10.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
                                                 Conservative
                                                                                                                                                                                                                                                            PRELIMINARY;
                                                                                                                                                                         140 LEECKNICED 149
                                                                                                                                                                                       |||::|::
132 EEECELVCKN 141
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
                                 Best Local Similarity
Matches 55; Conserv
                                                                                                                                                                                                                                                                                                                            Lacunin precursor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         52;
 SEQUENCE
                          Query Match
                                                                                                                                                                                                                                                                           Q9U8G8;
                                                                                                                                                                                                                                                            99866
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Matches
                                                                                                                                                                                                                                      RESULT 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        g
 g
                                                                                                                                                q
                                                                                                                                                                          δλ
                                                                                                                                                                                               qq
                                                                                                                                                                                                                                                                                                  δλ
                                                                                                Оp
                                                                                                                       á
```

```
ä
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1323 FVHGAQPSAARQEQAQPAAQPAQPAQPSNIVSPPQQSASPVVVPSNSKQRDACHLNVDQG 1382
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2436 YGGCHGGPNRFSTIDECQEVC------REEMDPCKQVVEPGDCTSRYVMMYX 2481
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Geisel C., Bradshaw H.;
"The sequence of C. elegans cosmid C37C3.";
Submitted (JUL-1996) to the EMBL/GenBank/DDBJ databases.
-!- ALTERNATIVE PRODUCTS: TWO FORMS (A AND B) MAY BE PRODUCED BY ALTERNATIVE SPLICING OF THE SAME GENE. THE SEQUENCE SHOWN IS THAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ---IIKTTLQQEKP------DFCFLEEDPG 104
56 YGGCEGNONRFESLEECKKMCTRDNANRIIKTTLQQEKPDFCFLEEDPGICRGYITRYFY 115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           18 PLKLMHSFCAFKADDGPCRAIMKRFFFNIFTRQCEEFIYGGCEGNQNRFESLEECKKMC- 76
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
Rhabditidae; Peloderinae; Caenorhabditis.
NCBI_TaxID=6239;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Prime, FF00090; tsp_1.6
PRINTS: PR00759; BASICPTASE.
PRINTS: PR00759; BASICPTASE.
SMART: SM00408; IGC2; 1.
SMART: SM00131; KU; 11.
SMART: SM00131; KU; 11.
PROSITE: PS00200; PFPI_KUNITZ_1; 10.
PROSITE: PS00200; TSP1; 4.
PROSITE: PS00209; Hypothetical protein; Immunoglobulin domain; Serine protease inhibitor.
MISSING (IN ISOFORM A).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 5; Length 2167;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  55; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       147 155 MISSING (IN ISOFORM A).
1556 1558 KDD -> SKF (IN ISOFORM A).
1559 2167 MISSING (IN ISOFORM A).
2167 AA: 237599 MW: 96274786D52E3639 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                105 ICRGYITRYFYNQQTKQCERFKYGGCLGNMNNFETLEECKNIC 147
                                                                                                                                                                                                                                                                                                                                                                                                          Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        29.4%; Score 266.5; DB 5
31.9%; Pred. No. 1.8e-20;
tive 23; Mismatches 55
                                                                                                                                                 2482 DNVRDTCLQFIYGGCHGNENFFTLEDCERKCRQRP 2517
                                                                                                                116 NQQTKQCERFKYGGCLGNMNNFETLEECKNICEDGP 151
                                                                                                                                                                                                                                                                                                                     PRT; 2167 AA
                                                                                                                                                                                                                                                                                                                                                                              Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL; U64857, AAC25868.1; -.
EMBL; U64857, AAC25867.1; -.
HSSP; POO981, 1DTK.
InterPro: IPR003508; Ig_c2.
InterPro: IPR003506; Ig_MHC.
InterPro: IPR003223; Kunitz_BPTI.
Pfam; PF00047; Ig; 1.
Pfam; PF00047; Ig; 1.
```

```
DDT BE SEED BY SEED BY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Вp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           97 ------CFLEEDPGI-C-RGYITRYFYNQQTKQCERFKYGGCLGNMNNFETLEECKN 145
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      844 GCCPSKAYTCSLQVNKGIGCGSGSSYRYYYNNQAKECQSYLFLGCDGNSNNFPSIEKCQN 903
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            786 FNSLNECQSYCKNINAEP--KCPQGRAYVDFSGKFMQCGEGLGGTACPANYECTFDGLVY 843
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               6 EEHTIITDTELPPLKLMHSFCAFKADDGPCRAIMKRFFFNIFTRQCEEFIYGGCEGNQNR 65
                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 28.6%; Score 258.5; DB 5; Length 1195; 31.6%; Pred. No. 7.5e-20; tive 26; Mismatches 45; Indels 59;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        "Genome sequence of the nematode C. elegans: a platform for investigating biology. The C. elegans Sequencing Consortium."; Science 282:2012-2018(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROW N.A.

STRAIN-BRISTOL N2;

Waterston R.;

Whitest Submission.";

Submitted (JUN-2001) to the EMBL/GenBank/DDBJ databases.

E Submitted (JUN-2001) to the EMBL/GenBank/DDBJ databases.

R EMBL; AC02480; ARF$9608.1; -.

R InterPro; IPR002223; Kunitz_BPTI.

R InterPro; IPR002223; Kunitz_BPTI.

R Pfam; PF001683; EB; 1.

R Pfam; PF001683; EB; 1.

R Pfam; PF00041; Kunitz_BPTI; 5.

R PRINTS; PR00759; BASTCPTASE.

R PRINTS; SM00131; KU1; 5.

R SMART; SM00131; KU1; 5.

R SMART; SM00139; WR1; 7.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PROSITE; PS00280; BPTI_KUNITZ_1; 1.
PROSITE; PS50279; BPTI_KUNITZ_1; 5.
Hypothetical protein; Serine protease inhibitor.
SEQUENCE 1195 Aa; 131342 MW; E77C3A6DF2272A18 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
STRAIN=BRISTOL N2;
Bradshaw-Cordum H., Leonard S., Graves T.;
"The sequence of C. elegans cosmid Y55F3BR.";
Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                     ou-OCT-2000 (TrEMBLrel. 15, Last sequence update)
U-JUN-2002 (TrEMBLrel. 21, Last annotation update)
Hypothetical 131.3 kba protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          66 FESLEECKKMCTRDNANRIIKTTLQQEKPDF-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRT; 1572 AA.
                                                                                                  PRT; 1195 AA
                                                                                                                                                                                                                                                                                                                                                                                                                  Rhabditidae, Peloderinae, Caenorhabditis.
NCBI_TaxID=6239;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STRAIN-BRISTOL N2;
MEDLINE-99069613; Pubmed-9851916;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRELIMINARY;
                                                                                                  PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                            Caenorhabditis elegans.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Best Local Similarity
Matches 60; Conserva
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             146 ICEDG--PNG 153
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       904 YCEIAICPNG 913
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   044938
                                                                                               Q9N343
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 8
044938
ID 04493
                                RESULT 7
                                                              Q9N343
                                                                                                          HID DE RECENT OF RECENT OF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             õ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ò
```

```
1436 SREECENTCVRHSEPHSDTTSHGTSVCDEAKETGPCTNFATKWYYNKADGTCNRFHYGGC 1495
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 "Cloning and characterization of thrombospondin, a novel multidomain glycoprotein associated with the gut of Haemonchus contortus."; submitted (MAR-201) to the EMBL/GenBank/DDBJ databases. EMBL, AF043121; AAB99830.2; --
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            60 EGNONRFESLEECKKMCTRDNANRIIKTTLQQEKPDFCFLEEDPGICRGYITRYFYNQQT 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 58; Indels 16; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2 SEEDEEHTIITDTELPPLKLMH--SFCAFKADDGPCRAIMKRFFFNIFTRQCEEFIYGGC 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
Rhabditidae; Peloderinae; Caenorhabditis.
                                                                                                                                                        Haemonchus contortus (Barber pole worm).
Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Strongylida;
Trichostrongyloidea; Haemonchidae; Haemonchinae; Haemonchus.
                                                                                                                                                                                                                                                                                                                                        STRAIN=MOREDUN;
Skuce P.J., Newlands G.F.J., Stewart M., Pettit D., Smith D.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 1572;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PROSITE; PS00280; BPTI_KUNITZ_1; 6.
PROSITE; PS50279; BPTI_KUNITZ_2; 6.
PROSITE; PS50020; TSP1; 2.
Serine protease inhibitor.
SEQUENCE 1572 AA; 171871 MW; 2260B30DC2F903EC CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Submitted (MAR-1997) to the EMBL/GenBank/DDBJ databases.
01-JUN-1998 (TrEMBLrel. 06, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-JUN-1998 (TrEMBLrel. 06, Last sequence update) 01-JUN-2002 (TrEMBLrel. 21, Last annotation update) W01F3.3 protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match

28.5%; Score 258; DB 5;
Best Local Similarity 35.6%; Pred. No. 1.1e-19;
Matches 53; Conservative 22; Mismatches 58
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRT; 2225 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1542 MSCEKFTYGGCLGNTNRFSTLDECQSRCQ 1570
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  120 KQCERFKYGGCLGNMNNFETLEECKNICE 148
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       06, Created)
06, Last sequ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  InterPro; IPR00561; EGF-like.
InterPro; IPR002223; Kunitz_BPTI.
InterPro; IPR00884; TSP1.
Pfam; PF00014; Kunitz_BPTI; 6.
Pfam; PF00014; Kunitz_BPTI; 6.
PRINTS; PR00759; BASICPTASE.
ProDom; PD000222; Kunitz_BPTI; 6.
SMART; SM00131; KU; 6.
SMART; SM00131; KU; 6.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
MEDLINE=99069613; PubMed=9851916;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-JUN-1998 (TrEMBLrel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Caenorhabditis elegans.
                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                                                                                                                                              NCBI_TaxID=6289;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NCBI_TaxID=6239;
                                                                                                   Thrombospondin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Cummings P.N.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WOLF3.3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            045881
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                045883
```

ë,

```
4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A Adams M.D., Celniker S.E., Holf R.A, Evans C.A., Gocayne J.D.,
A Adams M.D., Celniker S.E., Holf R.A, Evans C.A., Gocayne J.D.,
A Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
A Goorge R.A., Lewis S.E., Richards S., Ashburner M., Henglerson S.N.,
Bruton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Bandwin D.,
Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Besaley E.M.,
Besson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
Burtis R.C., Busam D.A., Buller H., Cadieu E., Center A., Chandra I.,
A Burtis R.C., Busam D.A., Buller H., Cadieu E., Center A., Chandra I.,
A Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
A de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
A Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
A Purbin K.J., Evangelista C.C., Ferrac C., Ferriera S., Fleischann W.,
A Fosler C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Drosophila melanogaster (Fruit fly).
Eukaryota, Medezaoa, Arthropoda, Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 DSEEDEEHTIITDTE------LPPLKLMHSF'-------CAFKADDGPC 35
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          36 RAIMKRFFFNIFTRQCEEFIYGGCEGNQNRFESLEECKKMCTRDNANRIIKTTLQQEKPD 95
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            96 F---CFLEEDPGICRGYITRYFYNQQTKQCERFKYGGCLGNMNNFETLEECKNIC 147
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       840 FSQVCSNDVDAGECNGVFERFAFDAEAQDCRAFTYGGCGGNGNNFATMQECRSRC 894
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DB 5; Length 2225;
                            'Genome sequence of the nematode C.elegans: A platform for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Serine protease inhibitor.
SEQUENCE 2225 AA; 242198 MW; A5DD8AE9D2A7B02A CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             28.5%; Score 257.5; DB 5 30.9%; Pred. No. 1.9e-19; iive 23; Mismatches 63
                                                                                                                                                                                                                                                                                                                                                          PRT; 3060 AA
                                                                                                                                                                                       Interpro; IPR00223; Kunitz_BPTI.
InterPro; IPR00213; Thyroglobulin_1.
InterPro; IPR002899; WR1/EB.
Pfam; PF00014; Kunitz_BPTI; 10.
Pfam; PF00086; thyroglobulin_1; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STRAIN-BERKELEY;
MEDLINE-20196006; PubMed-10731132;
                                                               investigating biology.";
Science 282.2012.2018(1998).
EmBL: 292815; CABO7294.1; -
HSSP; P31713; 1SHP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    54; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PPN OR CG1540 OR CG18436.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Ephydroidea; Dros
NCBI_TaxID=7227;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CG1540 protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Q9VAV4; Q9VAV3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Q9VAV4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       рp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          δλ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RATARTA RATARTA DE LA RATARTA 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ò
```

```
Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
A Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,
Jalali M., Kalush F., Karpen G.H., Ke Z., Kenlson J.A., Ketchum K.A.,
Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
A. Liu X., Mattei B., McIntosh T.C., Morios J., Moshrefi A.,
Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
Nelson D.K., Nelson K.A., Nixon K., Nussken D.R., Pacleb J.M.,
Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
Spier E., Siden Krämos I., Simpson M., Skropski M.P., Smith T.,
She B.C., Stadellung A.C., Stapleton M., Strong R., Sun E.,
Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
Williams S. M., Woodage T., Woilberton M., Weissenbach J.,
A. Walliams S. M., Woodage T., Woilber K., Wu D., Yang S., Yao Q., A.,
A. Lid Sheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
A. The genome sequence of Drosophila melanogaster."
B. Scheng R.A., Myers E.W., Rubin G.M., Venter J.C.,
B. Strandshamstyn Drongmen.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2021 ADPVEHDTSK - CFLAFEPGNCYNNVTRWFYNSAEGLCDEFVYTGCGGNANNYATEEECQN 2079
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      86 KITLQQEKPDFCFLEEDPGICRGYITRYFYNQQTKQCERFKYGGCLGNMNNFETLEECKN 145
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            26 CAFKADDGPCRAIMKRFFFNIFTRQCEEFIYGGCEGNQNRFESLEECKKMCTRDNANRII 85
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -!- ALTERNATIVE PRODUČTS: Ź ISOFORMS; A LONG FORM (SHOWN HERE) AND SHORT FORM; ARE PRODUCED BY ALTERNATIVE SPLICING.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   L -> SVVPV (IN SHORT ISOFORM).
FNFKTMEDSGI -> VASPPLHPNAV (IN SHORT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 28.1%; Score 254.5; DB 5; Length 3060; Best Local Similarity 40.3%; Pred. No. 5.6e-19; Matches 50; Conservative 17; Mismatches 56; Indels 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ISOFORM).
50 MISSING (IN SHORT ISOFORM).
331579 MW; ACA31D3EE558C7C0 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Alternative splicing; Immunoglobulin domain;
Serine protease inhibitor. L -> SVVPV (IN 9988)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PROSITE; PS00317; 4_DISULFIDE_CORE; 1. PROSITE; PS00280; BPT1_KUNITZ_1; 11. PROSITE; PS50279; BPT1_KUNITZ_2; 12. PROSITE; PS50092; EGF_1; UNKNOWN_1. PROSITE; PS50092; TSP1; 3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      HSSP, P12111; 2KNT.
FlyBase; FBGN0003137; Ppn.
InterPro: IPR0000511; EGF-like.
InterPro: IPR0005598; Ig_c2.
InterPro: IPR003598; Ig_c2.
InterPro: IPR003598; Ig_MHC.
InterPro: IPR002231; Kunitz_BPTI.
InterPro: IPR002221; WAP.
InterPro: IPR002221; WAP.
Ffam; PF00047; Ig; 3.
Ffam; PF000047; Ig; 3.
Ffam; PF000095; Wap; 1.
Ffam; PF000095; Wap; 1.
Fronom; PP000222; Kunitz_BPTI; 12.
SWART; SW00408; IGc2; 3.
SWART; SW00209; TSP1; 7.
SWART; SW00209; TSP1; 7.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL; AE003765; AAF56794.2; -. EMBL; AE003765; AAF56795.2; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            3060
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2854
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2855 306
3060 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2080 ECND 2083
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                146 ICED 149
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         VARSPLIC
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           VARSPLIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 a
                     $\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          δŏ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Ωp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ŏ
```

Ĥ

```
McMurray
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Q9GQR0
                                                                                                               none;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    09GOR0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AC OCC OCC OCC OCX NR RR RR RR RX RX RX
g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          임
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 δλ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      δŏ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            3;
                                                                                                                                                                                                                                                                                                                                                                                                       PROSITE; PS00010; ASX_HYDROXYL; 2.
PROSITE; PS00020; BPTI_KUNITZ_1; 2.
PROSITE; PS000279; BPTI_KUNITZ_2; 5.
PROSITE; PS00022: EGF_1; UNKNOWN_2.
PROSITE; PS01186; EGF_2; 6.
PROSITE; PS01187; EGF_CA; 2.
Calcium-binding; EGF-like domain; Glycoprotein; Hydroxylation; Repeat; Serine protease inhibitor.
Serine Protease inhibitor.
                                                                                                                                                                            TRAIN—BRIGGOL NJ.

STRAIN—BRIGGOL NJ.

MEDLINE=96158934; PubMed=8562083;

MEDLINE=96158934; PubMed=8562083;

MEDLINE=96158934; PubMed=8562083;

"Extracellular proteins needed for C. elegans mechanosensation.";

"Extracellular proteins needed for C. elegans mechanosensation.";

Neuron 16:183-194(1996).

REMBL; U33934; AAA96506.1; -.

REMBL; U33933; AAA96506.1; -.

REMBL; U33933; AAA96506.1; -.

REMBL; U33933; AAA96506.1; -.

REMBL; U33933; AAA96506.1; -.

REMBL; PRO00042; EGF_2.

RICEPPO; IPRO01262; EGF_1ike.

RICEPPO; IPRO0228; Kunitz_BPTI; 5.

Probom; PRO0008; EGF_6.

Probom; PRO000222; Kunitz_BPTI; 5.

REMART; SM000179; EGF_CA; 2.

REMART; SM000179; EGF_CA; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              69 LEECKKMCTRDNANRIIKTTLQQEKPDFCFLEEDPGIC---RGYITRYFYNQQTKQCERF 125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    79 KOOCVKOCKYKMFNPV-----AVPDLCLLDADQGHCGDERNGHWWYFFNQESGECEKF 131
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  11 ITDTELPP--LKLMHSFCAFKADDGPCRAIMKRFFFNIFTRQCEEFIYGGCEGNQNRFES 68
                                                                                                              Caenorhabditis elegans.
Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
Rhabditidae; Peloderinae; Caenorhabditis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    27.8%; Score 252; DB 5; Length 838;
35.9%; Pred. No. 2.7e-19;
Live 23; Mismatches 56; Indels 12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Last sequence update)
Last annotation update)
                                                                   Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        838 AA
                                 838 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Created)
                                                         Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               132 FYYGCGGNDNKFYSLHMCRKVC 153
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          126 KYGGCLGNMNNFETLEECKNIC 147
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-NOV-1996 (TrEMBLrel. 01, 01-JAN-1998 (TrEMBLrel. 05, 01-MAR-2002 (TrEMBLrel. 20, C50H2.3a protein.
                                                       01-NOV-1996 (TrEMBLrel. 01, 01-NOV-1996 (TrEMBLrel. 01, 01-MAR-2002 (TrEMBLrel. 20,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Best Local Similarity 35.99
Matches 51; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Caenorhabditis elegans.
                                 PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                SMART; SM00131; KU;
                                                                                                                                                                      SEQUENCE FROM N.A.
                                                                                                                                              NCBI_TaxID=6239;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Q18761
Q18761;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT 12
Q18761
              RESULT 11
                        027422
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Q
D
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AC DIT DIT OF OS OS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ò
                                              a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    δ
```

```
FUNDOUT SMOOT SEE CAR. 2.
SMART; SMOOT SEE CAR. 2.
SMART; SMOOT SEE CAR. 4.
PROSTIE; PSOOT SEE CAR. 4.
PROSTIE SEE CAR. 4.
PROST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Drosophila melanogaster (Fruit fly).
Brusaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Meoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            69 LEECKKMCTRDNANRIIKTTLQQEKPDFCFLEEDPGIC---RGYITRYFYNQQTKQCERF 125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 27.8%; Score 252; DB 5; Length 838; Best Local Similarity 35.9%; Pred. No. 2.7e-19; Matches 51; Conservative 23; Mismatches 56; Indels 12; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      11 ITDTELPP--LKLMHSFCAFKADDGPCRAIMKRFFFNIFTRQCEEFIYGGCEGNQNRFES 68
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
Rhabditidae; Peloderinae; Caenorhabditis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Genome sequence of the nematode C.elegans: A platform for
                                                                                                                                                                                                                                                                                                                                    Submitted (JUN-1996) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-MAR-2001 (TrEMBLrel. 16, Created)
01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
Extracellular matrix protein papilin precursor.
PPN OR CG1540 OR CG18436.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRT; 2174 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               investigating biology.";
Science 282:2012-2018(1998).
EMBL. 73971; CAA98251.1; -.
HSSP: P00743; ICCF.
InterPro; IPR0000152; Asx_hydroxyl.
InterPro; IPR00051; EGF_11ke.
InterPro; IPR000542; EGF_2.
InterPro; IPR001881; EGF_Ca.
InterPro; IPR001881; EGF_Ca.
InterPro; IPR001881; EGF_Ca.
Fram FP60008; EGF, 6.
Fram; PF00014; Kunitz_BPTI; 5.
PRINTS; PR00759; BASICPTASE.
PRODOM: PD0000222; Kunitz_BPTI; 5.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRAIN=DP CN BW;
MEDLINE=20530499; PubMed=11076767;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A. MEDLINE=99069613; Pubmed=9851916;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    132 FYYGCGGNDNKFYSLHMCRKVC 153
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               126 KYGGCLGNMNNFETLEECKNIC 147
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                         NCBI_TaxID=6239;
```

3;

```
Nature 368:32-38(1994).
                      SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          F30H5.3 protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NCBI_TaxID=6239;
                                                                                                                                                                                                                                                                                       Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           009983;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               009983
                                                                                                                                                                                                                                                                                                               Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 15
           QQ
                                                                                                                                                                                                                                                                                                                                                                                        δλ
                                                                                                                                                                                                                                                                                                                                                                                                                g
                                                                                                                                                                                                                                                                                                                                        ŏ
                                                                                                                                                                                                                                                                                                                                                                                                                                          ŏ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               3,
Kramerova I.A., Kawaquchi N., Nelson R.E., Fessler L.I., Chen Y., Kramerov A.A., Kusche-Gullberg M., Kramer J.M., Ackley B.D., Sieron A.L., Prockop D.J., Fessler J.H.; "Papilin in development; a pericellular protein with a homology to the ADAMTS metalloproteinases."; Development 17:5475-5485(2000). EMBL: AF205357; AAG37995.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 65 RFESLEECKKMCTRDNANRIIKTTLQQEKPDFCFLEEDPGICRGYITRYFYNQQTKQCER 124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           60; Indels 16; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DEEHTIITDTELPPLKLMHSFCAFKADDGPCRAIMKRFFFNIFTRQCEEFIYGGCEGNQN 64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Caenorhabditis elegans.
Eukaryota, Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
Rhabditidae; Peloderinae; Caenorhabditis.
NCBI_TaxID=6239;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DB 5; Length 2174;
                                                                                                                                                                                                                                                                                                                                                                                                                                                              POTENTIAL.
MW; 038F707952623120 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MCMurray A.A.;
Submitted (JUN-1996) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Matrix protein; Serine protease inhibitor; Signal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 27.4%; Score 248; DB 5; Best Local Similarity 31.8%; Pred. No. 2e-18; Matches 47; Conservative 25; Mismatches 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           922 AA.
                                                                                                                                                                                                                                                                                                                                                                                  PROSITE; PS00317; 4_DISULFIDE_CORE; 1. PROSITE; PS00280; BPTI_KUNIT2_1; 3. PROSITE; PS50279; BPTI_KUNIT2_2; 3. PROSITE; PS00022; EGF_1; UNKNOWN_1. PROSITE; PS50092; TSP1; 3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  125 FKYGGCLGNMNNFETLEECKNICEDGPN 152
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Created)
                                                                                                    Flybase; FBgn0003137; Ppn.
InterPro; IPR000561; EGF-11ke.
InterPro; IPR001559; Ig.
InterPro; IPR001598; Ig.
InterPro; IPR001500; Ig_like.
InterPro; IPR003006; Ig_MHC.
InterPro; IPR003006; Ig_MHC.
InterPro; IPR000223; Kunitz_BPTI.
InterPro; IPR000884; TSPI.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRT;
                                                                                                                                                                                                                                                                                               Kunitz_BPTI; 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         231936 MW;
                                                                                                                                                                                                                                                                     PRINTS; PR00003; 4DISULPHCORE.
PRINTS; PR00759; BASICPTASE.
                                                                                                                                                                                                                  Pfam; PF00047; ig; 2.
Pfam; PF00014; Kunitz_BPTI; 3.
                                                                                                                                                                                                                                                                                          ProDom; PD00022; Kunitz_BP1
SMART; SM00409; IG; 3.
SMART; SM00408; IGc2; 2.
SMART; SM00410; IG_like; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-NOV-1996 (TrEMBLrel. 01, 01-NOV-1996 (TrEMBLrel. 01, 01-JUN-2002 (TrEMBLrel. 21, K10D3.4 protein.
                                                                                                                                                                                                      InterPro; IPR002221; WAP.
                                                                                                                                                                                                                                                                                                                                                           SMART; SM00209; TSP1; 7.
                                                                                                                                                                                                                                               tsp_1; 5.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                 SMART; SM00410; IG_like
SMART; SM00131; KU; 3.
                                                                                                                                                                                                                                                                                                                                                                         SM00217; WAP: 1
                                                                                                                                                                                                                                                            ; wap; 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE 2174 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                                                                              PF00090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       021418;
                                                                                                                                                                                                                                                                                                                                                                         SMART;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          021418
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   K10D3.4
                                                                                                                                                                                                                                                                                                                                                                                                                                                               SIGNAL
                                                                                                                                                                                                                                              Pfam;
                                                                                                                                                                                                                                                           Pfam;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT 14
Q21418
      g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   δλ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    à
```

```
STRAIN=BRISTOL N2;
XX MEDLINE=94150718; Pubmed=7906398;
XM Wilson R., Ainscough R., Anderson K., Baynes C., Berks M.,
Milson R., Ainscough R., Anderson K., Baynes C., Berks M.,
Bonfield J., Burton J., Connell M., Copsey T., Cooper J., Coulson A.,
Bonfield J., Burton J., Connell M., Copsey T., Cooper J., Coulson A.,
A craxton M., Daar S., Du Z., Durbin R., Favello A., Fulton L.,
Jones M., Kershaw J., Kirsten J., Laister N., Latreille P.,
Lightning J., Lloyd C., McMurray A., Mortimore B., O'Callaghan M.,
Parsons J., Percy C., Rifken L., Roopra A., Saunders D., Shownkeen R.,
Smaldon N., Smith A., Sonnhamer E., Staden R., Sulston J.,
A Thierry-Mieg J., Thomas K., Vaudin M., Vaughan K., Waterston R.,
A witson A., Weinstock L., Wilkinson-Sproat J., Wohldman P.;
Lelegans J., Percy L., Rick R., Percy R., R., Percy R., R., Percy R., R., Percy R., Per
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      471 IQGTALTDSNGNFIICGGSSAASTTCPAN--HYCYYDGTTYGCCPTQAYTCSLSYKSGAS 528
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ---EDPGI 105
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Caenorhabditis elegans.
Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
Rhabditidae; Peloderinae; Caenorhabditis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            44;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              106 CRGYITRYFYNQQTKQCERFKYGGCLGNMNNFETLEECKNIC--EDGPNGFQV 156
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 922;
                                                            Genome sequence of the nematode C.elegans: A platform for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        26 CAFKADDGPCRAIMKRFFFNIFTRQCEEFIYGGCEGNQNRFESLEECKKMC-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PROSITE; PS00280; BPTI_KUNITZ_1; 2.
PROSITE; PS50279; BPTI_KUNITZ_2; 5.
Serine protease inhibitor.
SEQUENCE 922 AA; 99995 MW; OCCBBCOAE2524CFD CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-NOV-1996 (TrEMBLrel. 01, Last sequence update) 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              27.0%; Score 244; DB 5; 30.1%; Pred. No. 2.3e-18; Live 24; Mismatches 53
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           77 ----TRDNANRII-----KTTLQQEKPDFCFLE----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRT; 1599 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-NOV-1996 (TrEMBLrel. 01, Created)
                                                                                                                                                                                                                       InterPro; IPR002233; Kunitz_BPTI.
InterPro; IPR002299; WR1/EB.
Pfam; PF01683; EB; 1.
Pfam; PF0014; Kunitz_BPTI; 5.
PRINTS; PR00759; BASICPTASE.
PRODOM; PD000222; Kunitz_BPTI; 5.
SWART; SM00131; KU; 5.
MEDLINE=99069613; PubMed=9851916;
                                                                                                   investigating biology.";
Science 282:2012-2018(1998).
EMBL; 275545; CAA99886.1; --
HSSP; P31713; 18HP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Local Similarity 30.19
nes 52; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                [2]
SEQUENCE FROM N.A.
STRAIN-BRISTOL N2;
Pauley A., Stellyes L.;
```

ŝ

```
Ouery Match

26.6%; Score 240.5; DB 5; Length 1599;
Best Local Similarity 31.2%; Pred. No. 1e-17;
Matches 55; Conservative 21; Mismatches 49; Indels 51;
                                                            "The sequence of C. elegans cosmid F30H5."; Submitted (JUN-1995) to the EMBL/GenBank/DDBJ databases.
                                   Waterston R.;
Submitted (JUN-1995) to the EMBL/GenBank/DDBJ databases.
EMBL: U29096; AAA68408.1; -
HSSP; P10646; LADZ.
                     SEQUENCE FROM N.A. STRAIN-BRISTOL N2;
```

;

Search completed: December 2, 2002, 10:04:16 Job time : 61.6716 secs

102 DPGI-C-RGYITRYFYNQQTKQCERFKYGGCLGNMNNFETLEECKNICEDG--PNG 153

||:| 566 PLRL------GDCKQSVRRYWINAVTRACEIFDYTGCQGNDNNFFTLLECQNTCE 614 75 -----QEKPDFCFLEE 101

> Ω οy a δλ

18 PLKLMHSFCAFKADDGPCRAIMKRFFFNIFTRQCEFFIYGGCEGNQNRFESLEECKK--- 74

```
GenCore version 5.1.3
Copyright (c) 1993 - 2002 Compugen Ltd.
```

- protein search, using sw model OM protein December 2, 2002, 09:59:15 ; Search time 10.2985 Seconds Run on:

(without alignments)
297.593 Million cell updates/sec

US-09-741-106-10

114 1 KTKRKKKQRVKIAYEEIFVKNM 23 Perfect score:

Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

908470 seqs, 133250620 residues Searched:

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 08
Maximum Match 1008
Listing first 45 summaries

Database

A\_Geneseq\_101002:\*

// SIDS2/goddata/geneseq/geneseqp\_emb1/AA1989.DAT:\*
// SIDS2/goddata/geneseq/geneseqp\_emb1/AA1989.DAT:\*
// SIDS2/goddata/geneseq/geneseqp\_emb1/AA1990.DAT:\*
// SIDS2/goddata/geneseq/geneseqp\_emb1/AA1991.DAT:\*
// SIDS2/goddata/geneseq/geneseqp\_emb1/AA1992.DAT:\*
// SIDS2/goddata/geneseq/geneseqp\_emb1/AA1993.DAT:\*
// SIDS2/goddata/geneseq/geneseqp\_emb1/AA1995.DAT:\*
// SIDS2/goddata/geneseq/geneseqp\_emb1/AA1995.DAT:\*
// SIDS2/goddata/geneseq/geneseqp\_emb1/AA1995.DAT:\*
// SIDS2/goddata/geneseq/geneseqp\_emb1/AA1996.DAT:\*
// SIDS2/goddata/geneseq/geneseqp\_emb1/AA1998.DAT:\*
// SIDS2/goddata/geneseq/geneseqp\_emb1/AA1998.DAT:\*
// SIDS2/goddata/geneseq/geneseqp\_emb1/AA1998.DAT:\*
// SIDS2/goddata/geneseq/geneseqp\_emb1/AA1998.DAT:\*
// SIDS2/goddata/geneseq/geneseqp\_emb1/AA1998.DAT:\*
// SIDS2/goddata/geneseq/geneseqp\_emb1/AA2001.DAT:\* /SIDSZ/gogdata/geneseq/geneseqp-embl/AA1980.DAT:\*/SIDSZ/gogdata/geneseq/geneseqp-embl/AA1981.DAT:\*/SIDSZ/gogdata/geneseqg-embl/AA1981.DAT:\*/SIDSZ/gogdata/geneseqg-embl/AA1981.DAT:\*/SIDSZ/gogdata/geneseqg-embl/AA1984.DAT:\*/SIDSZ/gogdata/geneseqg-embl/AA1984.DAT:\*/SIDSZ/gogdata/geneseq/geneseqp-embl/AA1985.DAT:\*/SIDSZ/gogdata/geneseq/geneseqgp-embl/AA1985.DAT:\*/SIDSZ/gogdata/geneseqg-embl/AA1986.DAT:\*/SIDSZ/gogdata/geneseqg-embl/AA1987.DAT:\*/SIDSZ/gogdata/geneseqg-embl/AA1987.DAT:\*/SIDSZ/gogdata/geneseqg-embl/AA1988.DAT:\*/SIDSZ/gogdata/geneseqg-embl/AA1988.DAT:\*/SIDSZ/gogdata/geneseqg-embl/AA1988.DAT:\*/SIDSZ/gogdata/geneseqg-embl/AA1988.DAT:\*/SIDSZ/gogdata/geneseqg-embl/AA1988.DAT:\*/SIDSZ/gogdata/geneseqg-embl/AA1988.DAT:\*/SIDSZ/gogdata/geneseqg-embl/AA1988.DAT:\*/SIDSZ/gogdata/geneseqg-embl/AA1988.DAT:\*/SIDSZ/gogdata/geneseqg-embl/AA1988.DAT:\*/SIDSZ/gogdata/geneseqg-embl/AA1988.DAT:\*/SIDSZ/gogdata/geneseqg-embl/AA1988.DAT:\*/SIDSZ/gogdata/geneseqg-embl/AA1988.DAT:\*/SIDSZ/gogdata/geneseqg-embl/AA1988.DAT:\*/SIDSZ/gogdata/geneseqggeneseqg-embl/AA1988.DAT:\*/SIDSZ/gogdata/geneseqggeneseqg-embl/AA1988.DAT:\*/SIDSZ/gogdata/geneseqggeneseqg-embl/AA1988.DAT:\*/SIDSZ/gogdata/geneseqggeneseqg-embl/AA1988.DAT:\*/SIDSZ/gogdata/geneseqggeneseqg-embl/AA1988.DAT:\*/SIDSZ/gogdata/geneseqggeneseqg-embl/AA1988.DAT:\*/SIDSZ/gogdata/geneseqggeneseqggeneseqg-embl/AA1988.DAT:\*/SIDSZ/gogdata/geneseqggeneseqggeneseqggeneseqg-embl/AA1988.DAT:\*/SIDSZ/gogdata/geneseqggeneseqggeneseqggeneseqg-embl/AA1988.DAT:\*/SIDSZ/gogdata/geneseqgeneseqgeneseqggeneseqggeneseqggeneseqggeneseq 10: 

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

			Description		GT/COSCIIITION TACKII	Smooth musle fibre	TFPI C-terminal ta	Angiotensin conver	TFPI mutein, Lvs36	TFPI mutein K36R.	Recombinant non-al	Human tissue facto	Non-qlycosylated T	Human tissue facto
UMMARIES					,	01	53	32	55	1.2	[]	35	12	12
SUMM			ID	AAW06879	000	AAW21910	AAR9226	AAU0298	<b>AAR9226</b>	AAR9201	AAW30311	AAW61535	AAR37312	AAP92002
			DB	17	ł	18	17	22	17	17	18	13	14	10
			Match Length DB	23	1	23	37	161	276	276	276	276	277	304
	ф	Query	Match	1000		100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0
			Score	114		114	114	114	114	114	114	114	114	114
		Result	No.	-	١	7	m	4	S	9	7	8	6	10

14 16 AARB1884 14 16 AAR78389 14 16 AAR78389 14 21 AAY40572 14 21 AAY70273 15 17 AAR92011 16 18 AAW21912 18 AAW21924 19 18 AAW21924 19 18 AAW21924 10 18 AAW21924 10 18 AAW21921 11 AAR5881 11 AAR58117 11 AAR58117 12 AAR1117 13 AAR21913 14 18 AAW21913 15 AAR791913 16 AAW21913 17 AAR21913 18 AAW21913 19 AAW21913 11 AAW21913	3 0 0 4 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	Lipoprotein-associ Human Lipoprotein- Tissue factor path Human Lipoprotein Human mutant tissu	in-TFP ine pro musle musle	Smooth musle fibre Smooth musle fibre Smooth musle fibre Smooth musle fibre Smooth musle fibre	, n a n n n n n n	Smooth musle fibre Smooth musle fibre Human TPP1 heparin Smooth musle fibre Arabidopsis thalia Ser-(Aspl-11e253)- Smooth musle fibre Smooth musle fibre Smooth musle fibre	arrow
	3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3		AAR9201 AAR4230 AAW2192 AAW2191 AAR9226				AAM7215
		ннниии	нннн				101
01010101000000000000000000000000000000		1114 1114 1114 1114	114 113 109 108	107 103 100 99.5 98	888 881 72 72 64	ر ر <u>ب</u>	Š
1000001	1114 1114 1114 1117 1117 1117 1117 1117	112 12 13 14 15	17 18 19 20 21	22222 2222 22432	3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3	00000000000000000000000000000000000000	45

### ALIGNMENTS

```
Glycosaminoglycan binding peptide from TFPI.
       AA.
      AAW06879 standard; Peptide; 23
                    18-MAR-1997 (first entry)
             AAW06879;
RESULT 1
   AAW06879
```

Complement inhibitor; membrane co-factor protein; MCP; decay accelerating factor; DAF; chimeric protien; glycosaminoglycan; heparin; cell lysis; sepsis; adult respiratory distress syndrome; reperfusion injury; cell damage; tissue factor pathway inhibitor;

Synthetic.

WO9634965-A2

07-NOV-1996.

96WO-US06301 03-MAY-1996; 95US-0435149 05-MAY-1995;

(CHIR ) CHIRON CORP.

Ĥ Zaror Creasey AA, Innis MA,

WPI; 1996-506167/50.

Chimeric proteins for inhibiting complement-mediated cell lysis

```
;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Novel peptides contain: (a) a peptide sequence (P1) rich in basic amino acid residues (preferably lysine, arginine or histidine); and (b) a peptide sequence (P2) containing at least two consecutive hydrophobic amino acid residues (preferably phenylalanine, isolencine, leucine, methionine, proline, valine, tryptophan or tyrosine); where P2 is bound to the C-terminal end of P1 either directly or through a linker sequence of several amino acid residues. The peptides inhibit proliferation of smooth muscle cells, and are useful in the prevention and treatment of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Generic; TFPI; inhibitor; proliferation; smooth muscle cell; prevention; treatment; arteriosclerosis; restenosis; angioplasty; luminal stenosis; vascular transplantation; leiomyosarcoma; human.
                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Peptide(s) comprising basic rich peptide bound at C-terminal to consecutive hydrophobic rich peptide - useful for inhibiting smooth
                                                                                        A glycosaminoglycan binding peptide (AAW06879) derived from tissue factor pathway inhibitor is used in novel chimeric proteins of formula A-R1-B-R2-C, where A and C are peptides (AAW06875-79, AAW06883-90) capable of binding glycosaminoglycans (esp. heparin) present on cell surfaces, R1 is membrane co-factor protein (MCP) or decay accelerating factor (DAF), R2 is DAF when R1 is MCP or MCP when R1 is DAF, and B is a peptide that may have complement inhibitor activity. The chimeric proteins (see also AAW06882) are directed to cell surfaces where they inhibit complement-mediated cell lysis. They are used to treat and prevent disease states in which complement plays a role, e.g. sepsis, adult respiratory
comprise membrane co-factor protein and decay accelerating factor
                                                                                                                                                                                                                                                                                                                                                                                                                                ó;
                                                                                                                                                                                                                                                                                                                                                                                           Length 23;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Takemoto
                                                                                                                                                                                                                                                                                                                                                                                                                                Indels
                                                                                                                                                                                                                                                                                                               distress syndrome, reperfusion injury and tissue damage
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Smooth musle fibre proliferation inhibitor peptide 1.
                                                                                                                                                                                                                                                                                                                                                                                     100.0%; Score 114; DB 17;
100.0%; Pred. No. 3.7e-10;
ive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Miyamoto S, Nakahara Y,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (KAGA ) CHEMO-SERO-THERAPEUTIC RES INST.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAW21910 standard; peptide; 23 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 18; Page 22; 45pp; Japanese.
                                                        Claim 11; Page 26; 33pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 KTKRKRKKQRVKIAYEEIFVKNM 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 KTKKKKKKRKKORVKIAYEEIFVKNM 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             muscle fibre cell proliferation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           96WO-JP03080.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 95JP-0300792
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                            23; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Kamikubo Y,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 1997-258960/23.
                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity
                      peptide sequences
                                                                                                                                                                                                                                                                                                                                                   23 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         23-OCT-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WO9715598-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    14-JAN-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-MAY-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Synthetic.
                                                                                                                                                                                                                                                                                                                                                     Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAW21910;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Hara S,
                                                                                                                                                                                                                                                                                                                                                                                                                              Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT 2
AAW21910
οy
```

```
The sequences given in AAR92257-64 represent first, second and third
Kunitz-type domains and the C-terminal tails derived from tissue
factor pathway inhibitor (TPPI) and TPPI-2. These sequences are
inpuly basic and may be involved in cell surface localisation by
glycosaminoglycan (including heparin) or phospholipid binding.
These sequences may be used in the construction of the chimeric
proteins or muteins of the invention. These muteins have one or
more substitutions exclusively in the P1-reactive site of one or
more Kunitz-type domains. The chimeric proteins may comprise an
alternative glycosaminoglycan binding peptide selected from those
alternative glycosaminoglycan binding peptide selected from those
characterical composition for the treatment of sepsis, septic shock and
thrombosis disorders. The proteins may be generally useful in the
thrombosis disorders. The proteins may be generally useful in the
treatment of diseases caused by the up-regulation of tissue factor
bought on by injury, trauma, endotoxin, TNF, cancer, IL-1 or other
                                                                                                                                                                                    ó
                 restenosis after angioplasty, luminal stenosis after vascular transplantation, and leiomyosarcoma. AAW21910-12 are specific inhibitory peptides based on the generic Pl and P2 sequences shown in AAW21905 and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Kunitz-type domain; C-terminal tail; tissue factor pathway inhibitor; TFPI.7; TFPI-2; cell surface localisation; glycosaminoglycan; heparin; phospholipid; binding; chimeric protein; mutein; substitution; PI-reactive site; septis; septic shock; thrombosis; up-regulation; tissue factor; injury; trauma; endotoxin; TNF; cancer; IL-1; tumour necrosis factor; interleukin.
                                                                                                                                                                                      Gaps
arteriosclerosis associated with smooth muscle cell proliferation,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Chimeric protein comprising Kunitz-type domains from TFPI-1 and ... used for the treatment of septic shock and thrombosis disorders
                                                                                                                                                                                      ö
                                                                                                                                                   Length 23;
                                                                                                                                                                                      Indels
                                                                                                                                               100.0%; Score 114; DB 18;
100.0%; Pred. No. 3.7e-10;
ive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                              AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 10; Page 6; 68pp; English.
                                                                                                                                                                                                                         1 KTKKKKKÇRVKIAYEEIFVKNM 23
                                                                                                                                                                                                                                               1 KTKRKKKKQRVKIAYEEIFVKNM 23
                                                                                                                                                                                                                                                                                                                                                          AAR92263 standard; peptide; 37
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     95WO-US09464.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            94US-0286521
                                                                                                                                                                                                                                                                                                                                                                                                                                    (first entry)
                                                                                                                                                                     Local Similarity 100.
nes 23; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TFPI C-terminal tail.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (CHIR ) CHIRON CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 1996-129394/13.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AA;
                                                                                                              23 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             37
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            05-AUG-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WO9604378-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       25-JUL-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Creasey AA,
                                                                                                                                                                                                                                                                                                                                                                                                                                    30-SEP-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  15-FEB-1996.
                                                                                                                                                                                                                                                                                                                                                                                               AAR92263;
                                                                                                                Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence
                                                                                                                                                   Query Match
                                                                                                                                                                       Best Loca
Matches
                                                                                                                                                                                                                                                                                                                                        AAR92263
                                                                                                                                                                                                                                                          QQ
                                                                                                                                                                                                                                                                                                                                                                             δλ
 00000xx
```

δy Dp

161 AA;

Sequence

ö

```
ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Angiotensin converting enzyme splice variant; ACEV; interleukin 6; granulocyte colony stimulating factor receptor; glucagon; hypertrophy; platelet-derived endothedial cell growth factor; cardiovascular disease; cellular tumour antigen P53; cyclin-dependent kinase inhibitor 1C; vasoactive intestinal polypeptide receptor 2; arteriosclerosis; cancer; myocardial infarction; coronary arterial thrombosis; renal disease; dlabetic nephropathy; muscular disease; immune disorder; sarcoidosis; nultiple sclerosis; immune complex nephritis; deep vein thrombosis; nonarcoidotic pulmonary granulomatous disease; endothelial abnormality; vascular disorder; asbestosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Novel alternative splicing variants e.g. variant of angiotensin converting enzyme (ACEV), useful in identifying candidate compounds capable of binding to the variant and to detect anti-variant antibodies
                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Angiotensin converting enzyme (ACEV) splice variant protein #82.
                                                               .
0
   Length 37;
                                                            Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            David A, Azar I, Khosravi R, Bernstein J;
100.0%; Score 114; DB 17;
100.0%; Pred. No. 6.1e-10;
iive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                    AAU02982 standard; Protein; 161 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 4; Fig 82; 519pp; English.
                                                                                                                     1 KTKRKKKÇRVKIAYEEIFVKNM 23
                                                                                                                                                     15 KTKRKKKKQRVKIAYEEIFVKNM 37
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          17-NOV-2000; 2000WO-IL00766.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   99IL-0132978.
99IL-0133455.
                                                                                                                                                                                                                                                                                                                                                                                                                                                             (first entry)
                                                            Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (COMP-) COMPUGEN LTD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 2001-336004/35.
                         Best Local Similarity
Matches 23; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     N-PSDB; AAS06082.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WO200136632-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         17-NOV-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   10-DEC-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                             12-SEP-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                25-MAY-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Levine Z,
                                                                                                                                                                                                                                                                                                                                                                                                 AAU02982;
      Query Match
                                                                                                                                                                                                                                                                        RESULT 4
                                                                                                                                                                                                                                                                                                           AAU02982
```

The sequence represents an angiotensin converting enzyme splice variant (ACEV) polypeptide. The polypeptides of the invention include variants of granulocyte colony stimulating factor receptor, glucagon, interleukin 6, platelet-derived endothelial cell growth factor, cyclin-dependent kinase inhibitor IC, cellular tumour antigen P53, and vasoactive intestinal polypeptide receptor 2. The polypeptides and their associated nucleic acids are useful for identification of variant sequences and detection of candidate compounds capable of binding the molecules. The sequences of the invention can be used in the treatment and diagnosis of various consistence including cardiovascular diseases such as arteriosclerosis, myocardial infarction and coronary arterial thrombosis, renal diseases such as diabetic nephropathy, muscular diseases such as hypertrophy, immune disorders such as immune complex nephritis, multiple sclerosis, cancer, sarcoidosis, nonarcoidotic pulmonary granulomatous diseases such as asbestosis and vascular pathologies involving an endothelial

```
(TFPI). This sequence has a Lys to Arg mutation in the PI-reactive domain of the first Kunitz-type domain. The Kunitz-type domains are highly basic sequences and may be involved in cell surface localisation by glycosaminoglycan (including heparin) or phospholipid binding. Muteins such as this, having one or more substitutions exclusively in the PI-reactive site of one or more Kunitz-type domains are covered by the scope of the invention. Chimaric proteins comprising the kunitz-type domains from TFPI or TFPI-2, may also comprise an alternative glycosaminoglycan binding peptide selected from those given in ARR92266-73. The chimaric proteins and muteins may be used in a pharmaceutical composition for the treatment of sepsis, septic shock
                                                                                                                                                                                                                                                                                       Kunitz-type domain; C-terminal tail; tissue factor pathway inhibitor; TFPI: TFPI-2; cell surface localisation; glycosaminoglycan; heparin; phospholipid; binding; chimeric protein; mutein; substitution; PI-reactive site; sepsis; septic shock; thrombosis; up-regulation; tissue factor; injury; trauma; endotoxin; TNF; cancer; IL-1; tumour necrosis factor; interleukin.
                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      This sequence represents a mutein of tissue factor pathway inhibitor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Chimeric protein comprising Kunitz-type domains from TFPI-1 and -:
                              ..
   Length 161;
                                Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "Second Kunitz-type domain"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           "Third Kunitz-type domain"
100.0%; Score 114; DB 22;
100.0%; Pred. No. 2.8e-09;
iive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                    26..76
/note= "First Kunitz-type domain"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          "C-terminal tail"
                                                                                                                                                                                                                                                                                                                                                                                                                                    Location/Qualifiers
                                                                                                                                                                   AAR92265 standard; peptide; 276 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Disclosure; Page 8; 68pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /label= Lys36Arg
                                                                             139 KTKRKKKQRVKIAYEEIFVKNM 161
                                                             1 KTKKKKKÇRVKIAYEEIFVKNM 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    95WO-US09464.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  94US-0286521.
                                                                                                                                                                                                                                  (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /note= "T
240..276
                                Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           189..239
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ..147
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /note=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /note=
                                                                                                                                                                                                                                                                TFPI mutein, Lys36Arg.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Creasey AA, Innis MA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 1996-129394/13.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (CHIR ) CHIRON CORP.
              Local Similarity
tes 23; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                                       Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WO9604378-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    25-JUL-1995;
                                                                                                                                                                                                                                  30-SEP-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  05-AUG-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     15-FEB-1996.
                                                                                                                                                                                                   AAR92265;
 Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Domain
                              Matches
                                                                                                                                      RESULT 5
                                                                                                                                                      AAR92265
                                                             δ
                                                                                        Q
```

```
;
0
and thrombosis disorders. The proteins may be generally useful in the treatment of diseases caused by the up-regulation of tissue factor bought on by injury, trauma, endotoxin, TNF, cancer, IL-1 or other agents or conditions.
                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Production of tissue factor pathway inhibitor in yeast cells - with isolation from the insoluble cell fraction, used to treat or prevent
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Tissue factor pathway inhibitor; TFPI: TFPI-2; Factor-VIIa; Itssue factor: Factor-Xa; binding protein; tissue factor inhibitor; lipoprotein associated coagulation inhibitor; extrinsic pathway inhibitor; sepsis; septic shock;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A mutein (AAR92012) of tissue factor pathway inhibitor (TFPI) is prepd. by site-directed mutagenesis of an encoding sequence. In the mutein, the lysine residue in the Pl reactive site of the first Kunitz-type domain of TFPI is replaced by arginine. This domain is required for the inhibition of Factor-VIIa/tissue factor (TF) complex. The mutein may be expressed in Saccharomyces cerevisiae transformants, esp. as a ubiquitin fusion protein,
                                                                                                                                                                                                                                                                                                            ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 276;
                                                                                                                                                                                                                                                Length 276;
                                                                                                                                                                                                                                                                                                            Indels
                                                                                                                                                                                                                                            100.0%; Score 114; DB 17; 100.0%; Pred. No. 4.8e-09;
                                                                                                                                                                                                                                                                                                            .
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       100.0%; Score 114; DB 17;
100.0%; Pred. No. 4.8e-09;
Live 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   and as a Factor-VIIa/TF/Xa binding protein.
                                                                                                                                                                                                                                                                                                            Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAR92012 standard; Protein; 276 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Disclosure; Page 9; 36pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                         254 KTKRKRKKQRVKIAYEEIFVKNM 276
                                                                                                                                                                                                                                                                                                            ;
0
                                                                                                                                                                                                                                                                                                                                                                      1 KTKKKKKKQRVKIAYEEIFVKNM 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          95WO-US09377
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      94US-0286530
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Saccharomyces cerevisiae.
                                                                                                                                                                                                                                                                                                            Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             sepsis or septic shock
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Innis MA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 1996-129393/13.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (CHIR ) CHIRON CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Local Similarity
                                                                                                                                                                                                                                                                            Similarity
                                                                                                                                                                                276 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                276 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TFPI mutein K36R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WO9604377-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      05-AUG-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          25-JUL-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             08-MAY-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                15-FEB-1996.
                                                                                                                                                                                                                                                                                                            23;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          23;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence
                                                                                                                                                                                   Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAR92012;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
                                                                                                                                                                                                                                            Query Match
                                                                                                                                                                                                                                                                                Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Creasey
                                                                                                                                                                                                                                                                                                            Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAR92012
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Best
                            SSSSSXS
                                                                                                                                                                                                                                                                                                                                                                         à
                                                                                                                                                                                                                                                                                                                                                                                                                                g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME OF COLOR OF STATE OF STAT
```

```
This sequence represents the human tissue factor pathway inhibitor (TFPI) protein. TFPI is also known as Lipoprotein-associated coagulation inhibitor (LACI), extrinsic pathway inhibitor (EPI) and Tissue factor inhibitor (TFI). The DNA encoding this sequence was altered to contain the optimum codons for expression in E. coli, to allow for expression of this protein in the bacteria. TFPI is used in the aqueous formulation of the invention. The aqueous formulation also includes a charged polymer (CP), preferably a sulphated polyacocharide (such as heparin or dextran sulphate) or a polyphosphate, preferably immobilised on a soil support. The CP is added to add the correct refolding of TFPI. TFPI can also be modified or refolded using the methods of the invention. One method is for a CP to reduce inter- and intra-molecular interactions between the charged domains of the protein. The second method is for refolding an immobilise of denatured protein. TFPI is and comprises adding the a solution of the protein prior to allowing the protein to refold. The methods are particularly useful for solubilising, formulating,
                                                                                                                                                        Tissue factor pathway inhibitor; TFPI; human; tissue factor inhibitor; ilipoprotein-associated coagulation inhibitor; coagulation inhibitor; TFI; LACI; extrinsic pathway inhibitor; protein refolding; clot-inhibitor; protein solubility modification; EPI.
                                                                                                                                                                                                                                                                                                  /note= "phosphorylated to varying degrees, but does not
    affect TFPI function"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             charged polymer, e.g. dextran sulphate, to facilitate solubilisation, formulation purification and refolding of protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Aq. formulation of tissue factor pathway inhibitor - contains
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gustafson ME;
Johnson K, Madani H;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Chen B, Dorin GJ,
a MS, Johnson GV,
                                                                                                                                                                                                                                                                      Location/Qualifiers
                             AAW30311 standard; protein; 276 AA.
                                                                                                                           Recombinant non-glycosylated TFPI.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Disclosure; Fig 4; 86pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Hora MS, Journe
Pok. Tsang M;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      95US-0477677.
95US-0473668.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         96WO-US09980.
                                                                                           (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                             122..143
189..239
198..222
214..235
                                                                                                                                                                                                                                                                                                                                               35..59
51..72
97..147
106..130
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (CHIR ) CHIRON CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RF, HOLL
T Rana RK,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 1997-087056/08
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Bild GS,
                                                                                                                                                                                                                                                                                                                                                  Disulfide-bond
Disulfide-bond
Disulfide-bond
                                                                                                                                                                                                                                                                                                                                   Disulfide-bond
                                                                                                                                                                                                                                                                                                                                                                                                 Disulfide-bond
                                                                                                                                                                                                                                                                                                                                                                                                             Disulfide-bond
Disulfide-bond
                                                                                                                                                                                                                                                                                                                                                                                                                                              Disulfide-bond
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Disulfide-bond
                                                                                                                                                                                                                                                                      Key
Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WO9640784-A2.
                                                                                                                                                                                                                                         Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         07-JUN-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Pattison GL,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      07-JUN-1995;
07-JUN-1995;
                                                                                           30-JAN-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           19-DEC-1996.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Hallenbeck
                                                              AAW30311;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Arve BH,
              AAW30311
RESULT
```

.; 0

Gaps

Indels

254 KTKRKRKKQRVKIAYEEIFVKNM 276

1 KTKRKKKQRVKIAYEEIFVKNM 23

δ

Conservative

```
RESULT 9
                                                                                                                                                                                                                                                                                                                                                                                                                     Key
                                                                                                                                                                                                                                                     AAR37312
     g
                                                                                                                                                                                         δ
                                                                                             ö
purifying and refolding proteins (especially TFPI) which have been engineered by genetic recombination and produced in bacterial, yeast or other cells in a form that has a non-native tertiary structure. TFPI is a coagulation inhibitor which has clot-inhibiting properties.
                                                                                                                                                                                                                                                                    Human tissue factor pathway inhibitor; TFP1; TFP1-2; cell proliferation; angiogenesis-related disease; cancer; arthritis; macular degeneration;
                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Composition comprising tissue factor pathway inhibitor for inhibiting cell proliferation - for treating angiogenesis related
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note= "Kunitz-3 type protease inhibitor domain" 189.239
                                                                                                                                                                                                                                                                                                                                                                      note= "Kunitz-1 type protease inhibitor domain"
                                                                                                                                                                                                                                                                                                                                                                                                                         note= "Kunitz-2 type protease inhibitor domain"
                                                                                             .;
0
                                                                        Length 276;
                                                                                             Indels
                                                                                                                                                                                                                                                                                                                                                     'note= "Potential phosphorylation site"
                                                                       100.0%; Score 114; DB 18; 100.0%; Pred. No. 4.8e-09;
                                                                                             .;
0
                                                                                                                                                                                                                                                  Human tissue factor pathway inhibitor (TFPI).
                                                                                            Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                'note= "N-glycosylated"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note= "N-glycosylated"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  'note= "N-glycosylated"
                                                                                                                                                                                                                                                                                                                                  Location/Qualifiers
                                                                                                                                                                                        Ā
                                                                                                                            254 KTKRKKKQRVKIAYEEIFVKNM 276
                                                                                                                                                                                      AAW61535 standard; protein; 276
                                                                                                               1 KTKRKKKQRVKIAYEEIFVKNM 23
                                                                                             ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Papathanassiu AE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    98WO-US02699
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      97US-0796850
                                                                                                                                                                                                                             (first entry)
                                                                                            Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                              106..130
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              122..143
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           189..239
                                                                                                                                                                                                                                                                                                                                                                                                                                  ..147
                                                                                                                                                                                                                                                                                         diabetic retinopathy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (ENTR-) ENTREMED INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 1998-446947/38.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        167
                                                                                 Local Similarity
                                                    276 AA;
                                                                                                                                                                                                                                                                                                                                                                                             Disulfide-bond
Disulfide-bond
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Disulfide-bond
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Disulfide-bond
Disulfide-bond
                                                                                                                                                                                                                                                                                                                                                                                   Disulfide-bond
                                                                                                                                                                                                                                                                                                                                                                                                                                    Disulfide-bond
                                                                                                                                                                                                                                                                                                                                                                                                                                                Disulfide-bond
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Disulfide-bond
                                                                                                                                                                                                                                                                                                                                  Key
Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Modified-site
                                                                                                                                                                                                                                                                                                               Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            W09834634-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   06-FEB-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        06-FEB-1997;
                                                                                                                                                                                                                             06-NOV-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                13-AUG-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Green SJ,
                                                    Sequence
                                                                                                                                                                                                          AAW61535;
                                                                       Query Match
                                                                                                                                                                                                                                                                                                                                                                Domain
                                                                                                                                                                                                                                                                                                                                                                                                                  Domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Domain
                                                                                   Best Loc
Matches
                                                                                                                                                                          AAW61535
                                                                                                                                                                  RESULT
                                                                                                                                                                                               8888888
                                                                                                                 δ
                                                                                                                                   P
```

```
The present sequence represents the human tissue factor pathway inhibitor (FPPI). The invention provides compositions using TFPI and its homologs, e.g. TFPI-2 (AAM61586), for inhibiting cell proliferation. The compositions are claimed to be useful for inhibiting an anglogenesis-related disease, such as cancer, arthritis, macular
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Non-glycosylated; tissue factor pathway inhibitor; TFPI; multivalent; lipoprotein associated coagulation inhibitor; inhibitor; Kunitz-type; coagulation; domain; factor VIIa; LACI; tissue factor; factor Xa; complex; coagulation.
                                                                                                                                                                                                                                       Gaps
diseases e.g. cancer, arthritis, macular degeneration and diabetic retinopathy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  This sequence represents a non-glycosylated form of tissue factor
                                                                                                                                                                                                                                      ó
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Prodn. of non-glycosylated form of tissue factor pathway inhibitor in high yield - comprises culturing E.coli cells transformed with replication expression vector and subjecting isolated inclusion bodies to sulphitolysis or redn. with
                                                                                                                                                                                                          Length 276;
                                                                                                                                                                                                                                       Indels
                                                                                                                                                                                                         100.0%; Score 114; DB 19; 100.0%; Pred. No. 4.8e-09;
                                                                                                                                                                                                                                       ö
                                                                                                                                                                                                                                    0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Wun T;
                                                                                                                                               degeneration or diabetic retinopathy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 1; Column 15-18; 25pp; English.
                                             Claim 6; Pages 23-24; 37pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                       AA.
                                                                                                                                                                                                                                                                                AAR37312 standard; protein; 277
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gustafson ME,
                                                                                                                                                                                                                                                                 1 KTKKKKKÇRVKIAYEE1FVKNM 23
                                                                                                                                                                                        Query Match
Best Local Similarity 100.vv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   92US-0844297
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               92US-0844297
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         beta-mercapto-ethanol, etc.
                                                                                                                                                                                                                                                                                                                                                                                                                              (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Non-glycosylated TFPI.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 1993-175458/21.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (MONS ) MONSANTO CO
                                                                                                                                                                            276 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Escherichia coli.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Diaz-Collier JA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Disulfide-bond
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Disulfide-bond
Disulfide-bond
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Disulfide-bond
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Disulfide-bond
Disulfide-bond
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Disulfide-bond
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Disulfide-bond
                                                                                                                                                                                                                                                                                                                                                                                                                              20-SEP-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 02-MAR-1992;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               02-MAR-1992;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US5212091-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      18-MAY-1993.
                                                                                                                                                                                                                                                                                                                                                                                                   AAR37312;
                                                                                                                                                                             Sequence
```

```
.;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                          Human tissue factor inhibitor; TFI; human placenta lambda-P9 clone; basic protease inhibitor gene superfamily
pathway inhibitor (TFPI). TFPI is alternatively known as lipoprotein associated coagulation inhibitor (LACI). TFPI is a multivalent kunitz-type inhibitor of coagulation. The primary amino acid sequence of TFPI shows that it contains a highly negatively charged amino terminus, three tandem kunitz-type inhibitory domains and anity positively charged carboxyl terminal. The first kunitz domain of TFPI is needed for the inhibition of factor VIIa/Tissue factor complex and the second kunitz domian of TFPI is responsible for the inhibition of factor VIIa/Tissue factor is unknown. TFPI is thought to act in vivo to limit the initiation of coagulation by forming an inert, quaternary factor Xa:TFPI:factor
                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                       0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note= "Potential N-linked glycosylation site"
195..197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /note= "Potential N-linked glycosylation site"
31..53
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /note= "Potential N-linked glycosylation site"
                                                                                                                                                                                               Length 277;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /note= "Possible site for signal peptidase"
                                                                                                                                                                                                                      Indels
                                                                                                                                                                                              100.0%; Score 114; DB 14; 100.0%; Pred. No. 4.9e-09;
                                                                                                                                                                                                                         ..
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note= "See comments below"
153..16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         153..16
/note= "See comments below"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "See comments below"
                                                                                                                                                                                                                      Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1..28
/label= Signal_region
/note= "A-T rich"
28..29
                                                                                                                                                                                                                                                                                                                                                                                                                Human tissue factor inhibitor (TFI).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                      AAP92002 standard; protein; 304 AA.
                                                                                                                                                                                                                   0;
                                                                                                                                                                                                                                                              255 KTKRKRKKQRVKIAYEEIFVKNM 277
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Broze GJ, Kretzmer KK, Wun TC;
                                                                                                                                                                                                                                               1 KTKRKKKQRVKIAYEEIFVKNM 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 88EP-0870127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          87US-0123753
                                                                                                                                             VIIa:tissue factor complex.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (MONS ) MONSANTO CO (UNIW).
                                                                                                                                                                                                                                                                                                                                                                                        (first entry)
                                                                                                                                                                                                         Local Similarity 100.
nes 23; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 29..304
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                . 258
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 1989-159483/22.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 1969 N-PSDB; AAN90108.
                                                                                                                                                                     277 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Cleavage-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 22-JUL-1988;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          23-NOV-1987;
                                                                                                                                                                                                                                                                                                                                                                                        09-FEB-1990
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         31-MAY-1989
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EP318451-A.
                                                                                                                                                                      Sequence
                                                                                                                                                                                                                                                                                                                                                              AAP92002;
                                                                                                                                                                                              Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Region
                                                                                                                                                                                                                       Matches
                                                                                                                                                                                                                                                                                                              RESULT 10
                                                                                                                                                                                                                                                                                                                           AAP92002
   ò
                                                                                                                                                                                                                                                                       qq
```

```
Amino acid sequence of tissue factor inhibitor (TFI) cDNA isolate from lambda-P9 clone of human placenta cDNA library. Domains discerned include: highly negatively charged N-terminal; highly positively charged carboxy-terminal; intervening portion consisting of 3 homologous domains with sequences typical of Kunitz-type enzyme inhibitors. Based on homology study, it appears to be a member of the basic protease inhibitor gene superfamily. Sequences in misc. regions in feature table above have been independently confirmed by amino acid sequence analysis.
                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Kallikrein inhibiting proteins comprising a Kunitz domain homologous to bovine pancreatic trypsin inhibitor - useful for preventing or treating disorders attributable to excessive kallikrein activity, egg. in hereditary angloedema.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Lipoprotein-associated coagulation inhibitor; LACI; kallikrein; inhibitor; KIP; Kunitz domain; hereditary angloedema.
                                                                                                                                                                                                                                                                                        ö
                                                                                                                                                                                                                                                          Length 304;
                                                                                                                                                                                                                                                                                         Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Lipoprotein-associated coaqulation inhibitor (LACI).

    used in study of coagulation cascade for agents
    which inhibit factor Xa and Factor VIIA-TF

                                                                                                                                                                                                                                                          100.0%; Score 114; DB 10;
100.0%; Pred. No. 5.4e-09;
ive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /note= "Kunitz domain LACI-K2"
213..270
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        "Kunitz domain LACI-K1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /note= "Kunitz domain LACI-K3"
             DNA encoding human tissue factor inhibitor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1..28
/label= sig_peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                         AAR81884 standard; protein; 304 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Disclosure; Page 24; 46pp; English
                                                                     Claim 3; Figure 3; 14pp; English.
                                                                                                                                                                                                                                                                                                                                       282 KTKRKKKKRVKIAYEEIFVKNM 304
                                                                                                                                                                                                                                                                                                                     1 KTKRKKKQRVKIAYEEIFVKNM 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                94US-0208264.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     95WO-US00299
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (PROT-) PROTEIN ENG CORP.
                                                                                                                                                                                                                                                                                           Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ..178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Ladner RC, Markland W;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /note=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 1995-292934/38.
                                                                                                                                                                                                                                                                          Best Local Similarity
                                                                                                                                                                                                                                304 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WO9521601-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      11-JAN-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  10-MAR-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               11-JAN-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 18-MAR-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          17-AUG-1995
                                                                                                                                                                                                                                                                                         23;
                                                                                                                                                                                                                                   Sequence
                                                                                                                                                                                                                                                              Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Domain
                                                                                                                                                                                                                                                                                                                                                                                          RESULT 11
AAR81884
                                                                                                                                                                                                                                                                                           Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                     ò
```

0;

```
;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human; lipoprotein-associated coaqulation inhibitor; peptide library; inhibitor; plasmin; bovine; pancreatic trypsin inhibitor; Kunitz domain; fibrinolysis; fibrinogenolysis; bleeding; thrombolytic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The amino acid sequence of the human lipoprotein-associated coagulation inhibitor (LACI). The sequence encoding the K1 domain was used to generate a library of peptides which act as inhibitors of plasmin. The peptides (see ARR78390-R78599) are mutants homologous to bovine pancreatic trypsin inhibitor (BPTI) Kunitz domains that inhibit plasmin. The peptides can be used to prevent or treat a clinical condition exacerbated by plasmin e.g. inappropriate fibrinolysis or
            AAR81884 is the human lipoprotein-associated coagulation inhibitor LACI. The Kunitz domain, LACI-KI, of LACI is a kallikrein in inhibiting protein (KIP) upon which the claimed KIPs of the invention are based. The KIPs can be used for treating or preventing disorders
                                                                        attributable to excessive kallikrein activity, e.g. hereditary angioedema. The KIPs can also be used for assaying, purifying and in vivo imaging of kallikrein.
                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Novel plasmin inhibiting protein comprising a Kunitz Domain - useful to prevent/treat disorders attributable to excess plasmin activity.
                                                                                                                                                                                                     .
0
                                                                                                                                                                    Length 304;
                                                                                                                                                                                                     Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                  Human lipoprotein-associated coagulation inhibitor.
                                                                                                                                                                    100.0%; Score 114; DB 16;
100.0%; Pred. No. 5.4e-09;
Live 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note= "LACI-K1 domain"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /note= "LACI-K2 domain"
213..270
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /note= "LACI-K3 domain"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         'note= "signal peptide'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Disclosure; Page 28; 59pp; English.
                                                                                                                                                                                                                                                                                                                                        AAR78389 standard; protein; 304 AA.
                                                                                                                                                                                                                                                 1 KTKRKKKÇRVKIAYEEIFVKNM 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             95WO-US00298
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          94US-0208265.
                                                                                                                                                                                                                                                                                                                                                                                                   27-FEB-1996 (first entry)
                                                                                                                                                                    Query Match
Best Local Similarity 100.
Matches 23; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ..178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (PROT-) PROTEIN ENG CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       50..107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Markland W;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 1995-255042/33.
                                                                                                                                        304 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             11-JAN-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          10-MAR-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WO9518830-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        11-JAN-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              13-JUL-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Ladner RC,
                                                                                                                                                                                                                                                                                                                                                                      AAR78389;
                                                                                                                                        Sednence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Domain
                                                                                                                                                                                                                                                                                                           RESULT 12
                                                                                                                                                                                                                                                                                                                           AAR78389
                                                                                                                                                                                                                                                                                                                                                         X C C C C C C C X X
                                                                                                                                                                                                                                 δλ
                                                                                                                                                                                                                                                              Dp
```

```
ö
                                                                          ö
                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                         Yeast aspartic protease 3; YAP3; signal peptide; protein secretion; tissue factor pathway inhibitor; TFPI.
fibrinogenolysis, excessive bleeding associated with thrombolytics.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DNA construct encoding the yeast aspartic protease 3 signal peptide - provides improved secretion of proteins in transformed yeast cells, such as aprotinin and insulin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A Sall fragment encoding human tissue factor pathway inhibitor (TFPI) is given in AAQ81396. It was used to contruct expression vectors allowing production of TFPI in Saccharomyces cerevisee as fusions to the yeast aspartic protease 3 (TAPA) signal peptide, facilitating secretion of the recombinant TFPI.
                                                                          ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ;
0
                                                   304;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 304;
                                                 Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels
                                                                           Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  100.0%; Score 114; DB 16;
100.0%; Pred. No. 5.4e-09;
tive 0; Mismatches 0;
                                                                          ó
                                                100.0%; Score 114; DB 16; 100.0%; Pred. No. 5.4e-09;
                                                                                                                                                                                                                                                                                                                                                                 1..28
/label= Sig_peptide
/note= "TFPI signal peptide"
                                                        100.0%; Prea. ....
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Disclosure; Page 27-28; 56pp; English.
                                                                                                                                                                                                                                                                                                                                                     Location/Qualifiers
                                                                                                                                                                                       AAR67994 standard; Protein; 304 AA.
                                                                                                                282 KTKRKRKKQRVKIAYEEIFVKNM 304
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 282 KTKRKRKKQRVKIAYEEIFVKNM 304
                                                                                                                                                                                                                                                                Tissue factor pathway inhibitor
                                                                                                  1 KTKRKKKQRVKIAYEEIFVKNM 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 KTKKKKKÇRVKIAYEEIFVKNM 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Christiansen L, Petersen JG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            93DK-0000828.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     94WO-DK00281.
                                                                                                                                                                                                                                          (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 100.
Best Local Similarity 100.
Matches 23; Conservative
                                                                          23; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (NOVO ) NOVO-NORDISK AS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 1995-066903/09.
N-PSDB; AAQ81396.
                                                              Best Local Similarity
                          304 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            304 AA;
                                                                                                                                                                                                                                       13-AUG-1995
                                                                                                                                                                                                                                                                                                                               Homo saplens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   08-JUL-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            08-JUL-1993;
                                                                                                                                                                                                                                                                                                                                                                                                                  WO9502059-A
                                                                                                                                                                                                                                                                                                                                                                                                                                           19-JAN-1995
                                                                                                                                                                                                                 AAR67994;
                          Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence
                                                Query Match
                                                                                                                                                                                                                                                                                                                                                                 Peptide
                                                                          Matches
                                                                                                                                                               RESULT 13
                                                                                                                                                                            AAR67994
                                                                                                                          qq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             g
 SXCC
                                                                                                   ŏ
                                                                                                                                                                                                  δ
```

RESULT 14 AAY49557

```
Domain
                                                                                                                                                                                                                                                                                                                                                      Domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 humans
                                                            Region
                                                                                         Domain
                                                                                                                                                    Region
                                                                                                                                                                                                                                                      Region
                                                                                                                                                                                                                                                                                                                                                                                                      Region
          .
0
                                                                                                                                                                                                                                                                                                                                      AA232159 to AA232194 represent reference alleles for specifically claimed nucleic acid sequences from the present invention which comprise polymorphic sites as given in a table in the specification, selected from 9.2 single nucleotide polymorphisms in which the nucleotide at the polymorphic site is different from a nucleotide at the same site in a reference allele. The nucleic acids, and primers and probes, are used to identify polymorphisms, which may predispose an individual to disease, especially a vascular disease. They can also be used in phenotype correlations, forensics, paternity testing, medicine or genetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Tissue factor pathway inhibitor; TFPI; mutant; human; regulator; Kunitz-type proteinase inhibitor; extrinsic blood coagulation pathway; diagnosis; thrombotic disorder; thromboembolic disease.
                                                                                                                                                                                                                                                                                           Determination of polymorphisms in genes, especially those identifying
                                                                           Human; coding sequence polymorphism; vascular pathology gene; polymorphic site; phenotype correlation; forensic; paternity testing; medicine; genetic analysis; vascular disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                          Human lipoprotein associated coagulation inhibitor protein seguence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 304;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human mutant tissue factor pathway inhibitor protein (TFPI).
                                                                                                                                                                                                                                           Rozen SG;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               100.0%; Score 114; DB 20;
100.0%; Pred. No. 5.4e-09;
iive 0; Mismatches 0;
                                                                                                                                                                                                                                           Cargill M, Ireland JS,
                                                                                                                                                                                                                      (WHED ) WHITEHEAD INST BIOMEDICAL RES
                                                                                                                                                                                                                                                                                                     predisposition to vascular disease
                                                                                                                                                                                                                                                                                                                      Disclosure; Fig 10; 134pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAY70272 standard; Protein; 304 AA.
AAY49557 standard; Protein; 304 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                          to some of the reference alleles.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   282 KTKRKRKKQRVKIAYEEIFVKNM 304
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 KTKRKKKKQRVKIAYEEIFVKNM 23
                                                                                                                                                                               99WO-US06473.
                                                                                                                                                                                                   98US-0054272.
                                       (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 100.
Best Local Similarity 100.
Matches 23; Conservative
                                                                                                                                                                                                                                           Lander ES, Daley GQ,
                                                                                                                                                                                                                                                            WPI; 1999-620066/53.
                                                                                                                                                                                                                                                                                                                                                                                                                                                             304 AA;
                                                                                                                                                                                                                                                                        N-PSDB; AAZ32166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Homo sapiens.
                                                                                                                     Homo sapiens
                                                                                                                                       WO9950454-A2
                                                                                                                                                                               26-MAR-1999;
                                                                                                                                                                                                   01-APR-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   06-JUN-2000
                                      13-JAN-2000
                                                                                                                                                           07-0CT-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Seguence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAY70272;
g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ŏ
```

```
The present amino acid sequence is the mutant human tissue factor pathway inhibitor (FTPI) protein. A single nuclectide substitution (CTP) in exon 7 of the TFPI wild type gene, leads to a proline-leucine substitution in the mature peptide. TFPI is a single chain glycoprotein present in plasma in trace amounts, that belongs to the class of Kunitz-type proteinase inhibitors. It is an important regulator in the extrinsic blood coagulation pathway. The mutant TFPI sequence has a new recognition site for the restriction enzyme BseNI, that is useful for in vitro diagnosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          useful
                                                                                                                                                29..53
/label= Acidic_amino_terminal_region
/note= "Consists of negatively charged amino acids"
                                                                                                                                                                                                                   54..104
/label= Kunitz_type_proteinase_inhibitory_domain-1
/note= "Binding site for factor VIIa/tissue factor"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /label= Basic_carboxy_terminal_region
/note= "Consists of positively charged amino acids"
                                                                                                                                                                                                                                                                                                                                                                                                                 125..175
\tabel= Kunitz_type_proteinase_inhibitory_domain-2 \tabel= Ruids_activated factor Xa"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /label- Kunitz_type_proteinase_inhibitory_domain-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Polynucleotide encoding tissue factor pathway inhibitor mutant u for diagnosing a disposition for venous thromboembolic diseases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Schmidt M;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    'note= "Wild type Pro substituted with Leu"
                                                                                               /label= Mature_human_mutant_TFPI_protein
                                                                                                                        /note= "Tissue factor pathway inhibitor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Goetting C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     'note= "N-glycosylation site"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note= "O-glycosylation site"
203
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "O-glycosylation site"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           'note= "N-glycosylation site'
                                                                                                                                                                                                                                                                                             54..104
63..87
79..105
105..124
/note= "Connecting chain-1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      note- "Connecting chain-2"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Kleesiek K, Brinkmann T, Prohaska W,
                            ...28
'label= Signal_peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 10; Page 22-23; 27pp; English.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   99WO-EP06054
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 98EP-0115957
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            125..175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ..267
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ..158
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ..171
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ..267
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 2000-237617/20.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (KLEE/) KLEESIEK K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         N-PSDB; AAZ51316.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Misc-difference
                                                                                                                                                                                                                                                                                                Disulfide-bond
Disulfide-bond
Disulfide-bond
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Disulfide-bond
Disulfide-bond
Disulfide-bond
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Disulfide-bond
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WO200011034-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Disulfide-bond
Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Disulfide-bond
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 25-AUG-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                18-AUG-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  02-MAR-2000
                         Peptide
                                                                          Protein
```

of thrombotic disorders, especially thromboembolic diseases, by screening genomic DNA from blood samples. 8 × 6 6

Sequence 304 AA;

Query Match
100.0%; Score 114; DB 21; Length 304;
Best Local Similarity 100.0%; Pred. No. 5.4e-09;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps

ó

qq

Search completed: December 2, 2002, 10:02:23 Job time : 11.2985 secs

			•
			•

```
, Appl
, Appl
Appli
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Appl
Appl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Appli
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Appli
Appli
Appli
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Appli
Appli
Appli
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Appli
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Appli
Appli
Appli
Appli
Appli
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 10, Appl
Sequence 10, Appl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Appli
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Appli
                                                                                                                                                                                                       2, 2002, 10:02:30 ; Search time 3.77612 Seconds (without alignments) 179.212 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 10, Sequence 10, Sequence 11, Sequence 11, Sequence 11, Assequence 20, Sequence 20, Sequence 7, Assequence 11, Assequence 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 9, Sequence 9, Sequence 9, Sequence 1, Sequence 2, Sequence 2, Sequence 3, Sequen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 7, Sequence 1, Sequence 1, Sequence 9, Sequence 9, Sequence 9, Sequence 9,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 1,
Sequence 3,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 9,
Sequence 18
Sequence 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Description
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Issued_Patents_AA:*
1: /cgn2_6/ptodata/1/iaa/5A_COMB.pep:*
2: /cgn2_6/ptodata/1/iaa/5B_COMB.pep:*
3: /cgn2_6/ptodata/1/iaa/6A_COMB.pep:*
4: /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
5: /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
6: /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
GenCore version 5.1.3
Copyright (c) 1993 - 2002 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-08-437-841-10
US-08-286-521-10
US-08-436-175-110
US-08-9436-110
US-08-943-682-10
US-09-051-986-1
US-09-051-986-20
US-09-051-986-20
US-08-437-841-7
US-08-437-841-7
US-08-437-841-7
US-08-437-841-7
US-08-431-67-7
US-08-431-05-7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-07-828-920A-1
US-08-437-841-9
US-08-286-521-9
US-08-436-175-9
US-08-796-850-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PCT-US95-09464-9
US-07-844-297-1
US-08-026-145-2
US-08-446-646-9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US-08-676-125A-18
US-09-136-012A-18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PCT-US95-09377-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-08-854-764-3
US-08-943-682-9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          262574 segs, 29422922 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SUMMARIES
                                                                                                                                                                                                                                                                                                                                                                                                                         1 KTKRKKKQRVKIAYEEIFVKNM 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                                                                       OM protein - protein search, using sw model
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 BLOSUM62
Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Minimum DB seq length: 0
Maximum DB seq length: 200000000
                                                                                                                                                                                                                                                                                                                                                         US-09-741-106-10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query
Match Length DB
                                                                                                                                                                                                              December
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      100.0
100.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            100.0
100.0
100.0
100.0
100.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0.001
                                                                                                                                                                                                                                                                                                                                                  Title:
Perfect score:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Scoring table:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Database :
                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Searched:
                                                                                                                                                                                                           Run on:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Result
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              .
02
```

Appli Appli Appli Appli Appli Appli Appli Appli Appli Appli Appli Appli Appli Appli Appli Appli Appli Appli Appli			0
11, 11, 11, 12, 13, 11, 11, 11, 11, 11,			Gaps
Sequence Seq			;0
Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence			23;
Δ.			Length Indels
		30в	
11 25 25 25 25 25 25 25 25 25 25 25 25 25		# #	DB 1; 9e-10 0
US-08-676-124-1 US-09-2641-878-1 US-09-411-878-1 US-09-054-782-2 US-09-054-782-2 US-09-054-782-2 US-09-051-986-1 US-08-09-1-986-1 US-08-09-1-986-1 US-08-09-1-986-1 US-09-051-986-1 US-09-051-986-1 US-09-051-986-1 US-09-051-986-1 US-09-051-986-1 US-09-051-986-1 US-09-051-986-1 US-09-051-986-1 US-09-051-986-1 US-09-051-986-1 US-09-051-986-1 US-09-051-986-1	STN	s on	; DB 1.9e hes
676-676-676-676-676-676-676-676-676-676	ALIGNMENT	eins , Ver: 41	ced. No. 1.9 Mismatches
- 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	ALI	841 Prote #1.0, 37,84, 37,84,	Score Pred. Mism
		US/0843784; bla bla bla hael bla himeric Prc sorporation St. disk disk c-DoS/MS-Dc Release #1. TA: US/08/286, 105/08/286, 105. 105. 2585 105. 2585 105.	
www.d4460004444444		S/00 Indianal indianal indian	80.0
8 8 9 9 9 9 9 9 9 9 9 9 9 9 9 9 9 9 9 9		de le sincome a production de le sincome de la sincome de	100 larity 100 Conservative
000000000000000000000000000000000000000		Lication  23  TION:  Miss, Mic  TION:  ATTION:  CALLON:	ity serv
1000.0 10		1-10 WEORMATION: WEORMATION: WEORMATION: WE' Innis, Mic WE' Creasey, As WEORMATION: WE' SEGUENCES: NUDENCE ADDRESS SNEES: Chiron GO WE' A560 HOTTON EMERYVILE CA WY: USA 94608 WEATABLE FORM I TYPE: FLOPPY FRE, USA 94608 WE EADABLE FORM I TYPE: FLOPPY WE USA 94608 WE TAYPE: FLOPPY WE SEGUENCES: WEATABLE FORM I TYPE: BM PC COO! WE SEGUENCES: WEATABLE FORM I TYPE: BM PC COO! WE SEGUENCE WEATABLE WEATION WE SEGUENCE SAUGH UNICATION NUMBER: DATE: WEATION NUMBER: WEATION NUMBER: WEATION NUMBER: WEATION NUMBER: WEATION NUMBER: WEATION NUMBER: WE SEGUENCEST WEATION NUMBER: WE SEGUENCEST WE SEGUENCE	Similarity 3; Conser
11111111111111111111111111111111111111		ULT 1  08-437-841-10  dequence 10, Application atent No. 5563123  GENERAL INFORMATION: APPLICANT: Innis, Mi APPLICANT: Innis, Mi APPLICANT: Creasey, TITLE OF INVENTION: NUMBER OF SEQUENCES: CORRESPONDENCE ADDRES ADDRESSEE: Chiron STREET: 4560 Horto CITY: Emeryville STATE: CA COUNTRY: USA ZIP: 94608 COMPUTER: IBM PC COMPUTER: ILM COMPUTER: Savereide, PRESERRICE/DOCKET NO INFORMATION FOR SEQ ID SEQUENCE CHARACTERIST: TELEPHONE: 31 amino acid STRANDEDNESS: Sing: TOPOLOGY: linear MOLECULE TYPE: peptie	٦ 2
		1. 1 1-4.37-841	Match Local les 2
00000000000000000000000000000000000000		RESULT 1 US-08-437-841 Sequence 10 Sequence 10 Setent No. GENERAL IN APPLICAN TITLE OF NUMBER O CORRESPO ADDRES STREET CITL ZIP: CONTRES ZIP: CONTRES ZIP: CONTRES ZIP: CONTRES ZIP: CONTRES ZIP: ZIP: ZIP: ZIP: ZIP: ZIP: ZIP: ZIP:	Query M Best Lo Matches
		RS-SS	ÖÄÏ

ö

1 KTKKKKKQRVKIAYEEIFVKNM 23

δλ

```
Length 23;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                         SOFTWARE: Patentin Release #1.0, Version #1.30B CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Ouery Match
Best Local Similarity 100.0%; Pred. No. 1.9e-10;
Matches 23; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Innis, Michael
APPLICANT: Creasey, Abla
TITLE OF INVENTION: Chimeric Proteins
NUMBER OF SEQUENCES: 37
CORRESPONDENCE ADDRESS:
ADDRESSEE: Chiron Corporation
STREET: 4560 Horton St.
                                                                                                                                                   APPLICANT: Innis, Michael
APPLICANT: Creasey, Abla
TITLE OF INVENTION: Chimeric Proteins
NUMBER OF SEQUENCES: 37
CORRESPONDENCE ADDRESS:
ADDRESSEE: Chiron Corporation
STREET: 4560 Horton St.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: US/08/286,521
FILING DATE: 05-AUG-1994
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
RAME: SAVEREAGE, PAUL B.
REGISTRATION NUMBER: 36,914
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   100.0660
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                      ZIP: 94608
COMPUTER REALABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-08-436-175-10
; Sequence 10, Application US/08436175
; Patent No. 565608
; GENERAL INFORMATION:
                                                                                           Sequence 10, Application US/08286521 Patent No. 5589359
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            REFERENCE/DOCKET NUMBER: 0990
TELECOMMUNICATION INFORMATION:
TELEPHONE: 510-601-5285
TELEFAX: 510-655-3542
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 KTKRKKKKQRVKIAYEEIFVKNM 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 KTKRKKKKQRVKIAYEEIFVKNM 23
1 KTKKKKKKQRVKIAYEEIFVKNM 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         23 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             , MOLECULE TYPE: peptide US-08-286-521-10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              single
                                                                                                                                                                                                                                                                                                CITY: Emeryville STATE: CA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         amino acid
                                                                                                                                        GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         USA
                                                                                                                                                                                                                                                                                                                                         USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COUNTRY: US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ď
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TOPOLOGY:
                                                                              US-08-286-521-10
                                                                                                                                                                                                                                                                                                                                       COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STATE:
                                                              RESULT 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ó
```

```
0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 15, Application US/08435149
Fatent No. 5866402
GENERAL INFORMATION:
APPLICANT: INNIS, MICHAEL A.
APPLICANT: ZAROK, ISABEL
APPLICANT: CREASEY, ABLA A.
TITLE OF INVENTION: CHIMBRIC MCP AND DAF PROTEINS WITH CELL
TITLE OF INVENTION: SUFFACE LOCALIZING DOMAIN
NUMBER OF SEQUENCES: 26
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               100.0%; Score 114; DB 1; Length 23; 100.0%; Pred. No. 1.9e-10; Live 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ADDRESSEE: CHIRON CORPORATION
STREET: INTELLECTUAL PROPERTY - R440, P.O. BOX 8097
CITY: EMERYVILLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CURRENT APPLICATION DATA:
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/435,149
FILING DATE: 05-May-1995
CLASSIFICATION: 530
ATYONEY/AGENT INFORMATION:
NAME: SAVEREIDE, PAUL B.
REGISTRATION NUMBER: 36,914
REFRENCE/DOCKET NUMBER: 0989.001
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION 10F0RMATION:
TELEPRAS: (510) 601-2585
TELEFAX: (510) 655-3542
PatentIn Release #1.0, Version #1.30B
                                                                                                                                                                                                      TORNEY ACENT TO THE BOOK OF THE SAVETEIG, Paul B. REGISTRATION UNBER: 36,914
                    CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/436,175
FILING DATE: 09-MAY-1995
                                                                                                                   PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/286,521
FILING DATE: 05-AUG-1994
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                   REFERENCE/DOCKET NUMBER: 0990
TELECOMMUNICATION INFORMATION:
TELEPHONE: 510-601-2885
TELEFAX: 510-655-3542
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 23 aming acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 KTKRKRKKQRVKIAYEEIFVKNM 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 KTKKKKKKQRVKIAYEEIFVKNM 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  INFORMATION FOR SEQ ID NO: 15:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       23 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Best Local Similarity 100.0
Matches 23; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STATE: CALIFORNIA
COUNTRY: U.S.A.
ZIP: 94662-9097
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy di
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             , MOLECULE TYPE: peptide US-08-436-175-10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: amino acid
                                                                                               CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STRANDEDNESS:
     SOFTWARE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 4
US-08-435-149-15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
```

```
APPLICANT: NAKAHARA, YO
                                                                                                                                                                                                                                                                                                              TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                  Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                      δy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       g
                                                                                                               ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ;
0
                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                               .;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ;
0
                                                                             Length 23;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                100.0%; Score 114; DB 4; Length 23; 100.0%; Pred. No. 1.9e-10;
                                                                   Query Match 100.0%; Score 114; DB 2; Length 2 Best Local Similarity 100.0%; Pred. No. 1.9e-10; Matches 23; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SOFTWARE: Patentin Release #1.0, Version #1.30B CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/943,682 FILING DATE: 03-OCT-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0; Mismatches
                                                                                                                                                                                                                                                                                                                APPLICANT: Innis, Michael
APPLICANT: Creasey, Abla
TITLE OF INVENTION: Chimeric Proteins
NUMBER OF SEQUENCES: 37
CORRESPONDENCE ADDRESS:
ADDRESSEE: Chiron Corporation
STREET: 4560 Horton St.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: US 08/438,184
FILING DATE: 09-MX-1995
APPLICATION NUMBER: US 08/286,521
FILING DATE: 05-AUG-1994
ATTORNEY/AGENT INFORMATION:
NAME: Savereide, Paul B.
REGISTRATION NUMBER: 36,914
REFENDE/DCCKET NUMBER: 0990.001
TELECOMMUNICATION:
TELECOMMUNICATION:
TELEPHONE: 510-601-2585
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                Sequence 10, Application US/08943682
Patent No. 6174721
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 1, Application US/09051986A Patent No. 6191113
                                                                                                                                                           1 KTKRKKKQRVKIAYEEIFVKNM 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 KTKRKKKKRKKORVKIAYEEIFVKNM 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEFAX: 510-655-3542 INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 100.(
Matches 23; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LENGTH: 23 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              510-655-3542
                  ; MOLECULE TYPE: protein US-08-435-149-15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRIOR APPLICATION DATA:
APPLICATION NUMBER: U
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; MOLECULE TYPE: peptide US-08-943-682-10
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COUNTRY: US
                                                                                                                                                                                                                                                                                                                                                                                                                                                             S
                                                                                                                                                                                                                            RESULT 5
US-08-943-682-10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT 6
US-09-051-986-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                             STATE:
                                                                                                                                         Qγ
                                                                                                                                                                          g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    δ
```

```
Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         .;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 23;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 23;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SOFTWARE: Patentin Release #1.0, Version #1.30B CURRENT APPLICATION DATA: PCT/US95/09464 FILING DATE: PCT/US95/09464 CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                     100.0%; Score 114; DB 4;
100.0%; Pred. No. 1.9e-10;
Live 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
100.0%; Score 114; DB 5;
Best Local Similarity 100.0%; Pred. No. 1.9e-10;
Matches 23; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                    ; ORGANISM: Human Tissue Factor Pathway Inhibitor US-09-051-986-1
APPLICANT: HARA, SEQUED
APPLICANT: KAMIKUBO, YULCHI
APPLICANT: TAKMIKUBO, YULCHI
APPLICANT: TAKMIKUBO, SUMIYO
APPLICANT: MIYAMOTO, SUMIYO
APPLICANT: MIYAMOTO, SELI1
TITLE OF INVENTION: NOVEL PEPTIDE
FILE REFERENCE: NAKAHARA-I
CURRENT APPLICATION NUMBER: US/09/051,986A
CURRENT FILING DATE: 1998-104-24
EARLIER FILING DATE: 1998-10-24
EARLIER PELING DATE: 1996-10-24
EARLIER FILING DATE: 1996-10-24
EARLIER FILING DATE: 1996-10-23
NUMBER OF SEQ ID NOS: 26
NUMBER OF SEQ ID NOS: 26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Chimeric Proteins
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0990.100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 10, Application PC/TUS9509464
GENERAL INFORMATION:
APPLICANT: CHIRON CORPORATION
TITLE OF INVENTION: Chimeric Prote:
NUMBER OF SEQUENCES: 37
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Chiron Corporation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 KTKRKKKKQRVKIAYEEIFVKNM 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 KTKKKKKQRVKIAYEEIFVKNM 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ATTORNEY AGENT INFORMATION:
NAME: Savereide, Paul B.
REGISTRATION NUMBER: 36,914
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             REFERENCE/DOCKET NUMBER: 09
TELECOMMUNICATION INFORMATION:
TELEPHONE: 510-601-2585
TELEFAX: 510-655-3542
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELEFAX: 510-655-3542
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Best Local Similarity 100.
Matches 23; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STREET: 4560 Horton St
CITY: Emeryville
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LENGTH: 23 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   94608
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PCT-US95-09464-10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COUNTRY:
                                                                                                                                                                                                                                                                                                SEQ ID NO 1
```

GENERAL INFORMATION:

```
; Sequence 7, Application US/08436175
510-601-2585
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; MOLECULE TYPE:
US-08-286-521-7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       94608
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TOPOLOGY:
TELEPHONE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    23;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STATE: CA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT 11
US-08-436-175-7
                                                                                                                                                                                                                                                                                                                                                                                                                         US-08-286-521-7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STREET:
                                                                                                                                                                                                                       Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Matches
                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                δλ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    qq
                                                                                                                                                                                                                                                                                                        õ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              100.0%; Score 114; DB 4; Length 24; 100.0%; Pred. No. 2e-10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SOFTWARE: Patentin Release #1.0, Version #1.30B CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; TYPE: PRT
; ORGANISM: Human Tissue Factor Pathway Inhibitor
US-09-051-986-20
                                                                                                                                                                                                                                                                                 AFFLICANT: MIYAMOTO, Seliji
TITLE OF INVENTION: NOVEL PEPTIDE
FILE REPERENCE: NAKAHARA-1
CURRENT APPLICATION NUMBER: US/09/051,986A
CURRENT FILING DATE: 1998-04-24
EARLIER APPLICATION NUMBER: UP 300792/1995
EARLIER FILING DATE: 1995-10-24
EARLIER FILING DATE: 1995-10-24
EARLIER FILING DATE: 1996-10-23
NUMBER OF SEQ ID NOS: 26
SOFTWARE: PATENTIN UNBER: PCT/JP96/03080
SOFTWARE: PATENTIN UNBER: PCT/JP96/03080
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Innis, Michael
APPLICANT: Creasey, Abla
TITLE OF INVENTION: Chimeric Proteins
UNMER OF SEQUENCES: 37
CORRESPONDENCE ADDRESS:
ADDRESSEE: Chiron Corporation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME: Savereide, Paul B.
REGISTRATION NUMBER: 36,914
REFERENCE/DOORET NUMBER: 0990.001
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/286,521
FILING DATE: 05-AUG-1994
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: US/08/437,84
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COUNTRY: USA
ZIP: 94608
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC COMPATIBLE
COMPUTER: PC COMPATIBLE
COMPUTER: PC COMPATIBLE
COMPUTER: PC COMPATIBLE
COMPUTER: PC COMPA
                                                                                                                                              Sequence 20, Application US/09051986A
Patent No. 6191113
GENERAL INFORMATION:
APPLICANT: NAKAHARA, YO
APPLICANT: HARA, Saburo
APPLICANT: TAKEMOTO, Yuichi
APPLICANT: TAKEMOTO, Sumiyo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 7, Application US/08437841 Patent No. 5563123 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2 KTKRKRKKQRVKIAYEEIFVKNM 24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 KTKRKKKÇRVKIAYEEIFVKNM 23
                               1 KTKRKKKKQRVKIAYEEIFVKNM 23
          1 KTKRKKKKQRVKIAYEEIFVKNM 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STREET: 4560 Horton St. CITY: Emeryville STATE: CA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Best Local Similarity 100.
Matches 23; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FILING DATE
                                                                                                            RESULT 8
US-09-051-986-20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-08-437-841-7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQ ID NO 20
LENGTH: 24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ò
            δ
                                                qq
```

```
ö
                                                                                                                                                                                                                          ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ó
                                                                                                                                                                                                                          ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 37;
                                                                                                                                                                                    100.0%; Score 114; DB 1; Length 37; 100.0%; Pred. No. 3.1e-10; Live 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
OPEWARE: PATENTIN Release #1.0, Version #1.30B
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/286,521
FILING DATE: 05-AUG-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      100.0%; Score 114; DB 1; 100.0%; Pred. No. 3.1e-10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mismatches
                                                                                                                                                                                                                                                                                                                                                                                   Sequence 7, Application US/08286521
Patent No. 558959
GENERAL INFORMATION
APPLICANT: Innis, Michael
APPLICANT: Creasey, Abla
TITLE OF INVENTION: Chimeric Proteins
NUMBER OF SEQUENCES: 37
CORRESPONDENCE ADDRESS:
ADDRESSEE: Chiron Corporation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0990.001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 KTKRKKKÇRVKIAYEEIFVKNM 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     15 KTKRKRKKQRVKIAYEEIFVKNM 37
                                                                                                                                                                                                                                                                                   15 KTKRKRKKQRVKIAYEEIFVKNM 37
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0;
                                                                                                                                                                                                                                                                1 KTKKKKKKQRVKIAYEEIFVKNM 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ATTORNEY/AGENT INFORMATION:
NAME: Savereide, Paul B.
REGISTRATION NUMBER: 36,914
REFERENCE/DOCKET NUMBER: 099
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELECOMMUNICATION INFORMATION:
TELEPHONE: 510-601-2585
TELEFAX: 510-655-3542
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEFAX: 510-655-3542 INFORMATION FOR SEQ ID NO: 7: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               37 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          4560 Horton St
                                                                                                                                                                                                            Best Local Similarity 100.
Matches 23; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   peptide
                                                                                                        ; TOPOLOGY: linear;
; MOLECULE TYPE: peptide
US-08-437-841-7
                                                                                   TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Emeryville
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FILING DATE: 05 CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                USA
```

```
03-OCT-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COUNTRY: US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                               TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PCT-US95-09464-7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PCT-US95-09464-7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LENGTH:
                                                                                                                                                                                                                                                                                                    LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    qq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 37;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STATE: CA
COUNTRY: USA
ZIP: 94608
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.30B
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/943,682
                                                                                                                                                                                                                        ZIP: 94608
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Ploppy disk
COMPUTER: PROC COMpatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30B
CURRENT APPLICATION DATA:
APPLICATION UNMBER: US/08/436,175
FILING DATE: 09-MAY-1995
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
100.0%; Score 114; DB 1;
Best Local Similarity 100.0%; Pred. No. 3.1e-10;
Matches 23; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Innis, Michael
APPLICANT: Creasey, Abla
TITLE OF INVENTION: Chimeric Proteins
NUMBER OF SEQUENCES: 37
ADDRESSEE: Chiron Corporation
STREET: 4560 Horton St.
               GENERAL INFORMATION:
APPLICANT: Innis, Michael
APPLICANT: Creasey, Abla
TITLE OF INVENTION: Chimeric Proteins
NUMBER OF SEQUENCES:
CORRESPONDENCE ADDRESS:
ADDRESSEE: Chiron Corporation
                                                                                                                                                                                                                                                                                                                                                                                                               PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/286,521
FILING DATE: 05-AUG-1994
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 7, Application US/08943682
Patent No. 6174721
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               REFERENCE/DOCKET NUMBER: 0990
TELECOMMUNICATION INFORMATION:
TELEPHONE: 510-601-2885
TELEPAX: 510-655-3542
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 37 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 KTKRKKKÇRVKIAYEEIFVKNM 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               15 KTKKKKKKQRVKIAYEEIFVKNM 37
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME: Savereide, Paul B. REGISTRATION NUMBER: 36,914
                                                                                                                                                 STREET: 4560 Horton St
CITY: Emeryville
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; MOLECULE TYPE: peptide US-08-436-175-7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STREET: 4500...
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: amino acid
STRANDEDNESS: si
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GENERAL INFORMATION:
                                                                                                                                                                                                              USA
 Patent No. 5696088
                                                                                                                                                                                          S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TOPOLOGY:
                                                                                                                                                                                      STATE: C. COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-08-943-682-7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           δλ
```

```
Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   100.0%; Score 114; DB 5; Length 37; 100.0%; Pred. No. 3.1e-10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 37;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SOFTWARE: Patentin Release #1.0, Version #1.30B
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                    100.0%; Score 114; DB 4;
100.0%; Pred. No. 3.1e-10;
tive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 7. Application PC/TUS9509464
GENERAL INFORMATION:
APPLICANT: CHIRON CORPORATION
TITLE OF INVENTION: Chimeric Proteins
NUMBER OF SEQUENCES: 37
CORRESPONDENCE ADDRESS:
ADDRESSEE: Chiron Corporation
STREET: 4560 Horton St.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ATTORNEY/AGENT INFORMATION:
NAME: Savereide, Paul B.
REGISTRATION NUMBER: 36,914
REERENCE/DOCKET NUMBER: 0990.100
TELECOMMUNICATION INFORMATION:
TELEPHONE: 510-651-3542
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/438,184
APPLICATION NUMBER: US 08/286,521
FILING DATE: 05-AGC-194
ATTORNEY AGENT INFORMATION:
NAME: Savereide, Paul B.
REGISTRATION NUMBER: 36,914
REFERENCE/DOCKET NUMBER: 0990.001
TELEPHONE: 510-601-2585
TELEPHONE: 510-65-3542
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PCT/US95/09464
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 KTKKKKKKQRVKIAYEEIFVKNM 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           15 KTKRKRKKQRVKIAYEEIFVKNM 37
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                25-JULY-1995
                                                                                                                                                                                                                                                                                                              1: 37 amino acids amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           37 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEFAX: 510-655-3542
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   single
                                                                                                                                                                                                                                                                                                                                                  STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                       ; MOLECULE TYPE: peptide US-08-943-682-7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER:
FILING DATE: 25-JUL
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity
Matches 23; Conserva
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                           linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        linear
```

```
APPLICANT: Rasmussen, Jesper
APPLICANT: No. 5312736dfang, Ole Juul
APPLICANT: No. 5312736dfang, Ole Juul
TITLE OF INVENTION: Anticoagulant Protein
NUMBER OF SEQUENCES:
CORRESPONDENCE ADDRESS:
ADDRESSEE: No. 53127360 No. 5312736disk of No. 5312736th America, Inc.
STREET: 405 Lexington Avenue, Suite 6200
     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
     ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 276;
    Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels
                                                                                                                                                                                                                                                                       ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    100.0%; Score 114; DB 1;
100.0%; Pred. No. 2.3e-09;
tive 0; Mismatches 0;
  0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     30335
FR: 3287.204-US
                                                                                                                        Sequence 1, Application US/07828920A Patent No. 5312736 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       100.08; Pic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            254 KTKRKKKQRVKIAYEEIFVKNM 276
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 9, Application US/08437841
Patent No. 5563123
GENERAL INFORMATION:
                         NAME: Zelson, Steve T.
REGISTRATION NUMBER: 30335
REFERENCE/DOCKET NUMBER: 3287
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212 867 0123
TELEFAX: 212 867 0298
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 KTKRKKKÇRVKIAYEEIFVKNM 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 276 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LENGTH: 276 amino acids
TYPE: AMINO ACID
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Innis, Michael
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ORGANISM: Homo sapiens
  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Best Local Similarity 100.
Matches 23; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MOLECULE TYPE: protein ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME/KEY: Protein
LOCATION: 1..276
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            linear
                                                                                                                                                                                                                                                               New York
23;
                                                                                                            US-07-828-920A-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-07-828-920A-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-08-437-841-9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FEATURE
 Matches
                                                                                                RESULT 14
                            δy
                                                     g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ò
```

```
ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 100.0%; Score 114; DB 1; Length 276; 100.0%; Pred. No. 2.3e-09; tive 0; Mismatches 0; Indels (
                                                                                                                                                                                                                                                                                          SOFTWARE: Patentin Release #1.0, Version #1.30B CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/437,841
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Search completed: December 2, 2002, 10:05:57 Job time: 4.77612 secs
APPLICANT: Creasey, Abla
TITLE OF INVENTION: Chimeric Proteins
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME: Savereide, Paul B.
RECISTRATION NUMBER: 36,914
REFERENCE/DOCKET NUMBER: 0990.001
TELECOMMUNICATION INFORMATION:
TELEPHONE: 510-601-2585
                                                                                                                                                                                                                                                                                                                                                                                              PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/286,521
FILING DATE: 05-AUG-1994
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                         NUMBER OF SEQUENCES: 37
CORRESPONDENCE ADDRESS:
ADDRESSEE: Chiron Corporation
STREET: 4560 HORTON St.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 KTKRKKKKQRVKIAYEEIFVKNM 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEFAX: 510-655 3342
INFORMATION FOR SEQ ID NO: 9: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           276 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; MOLECULE TYPE: peptide US-08-437-841-9
                                                                                                                                                                                                              COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity
Matches 23; Conserva
                                                                                                                              Emeryville
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                               CLASSIFICATION:
                                                                                                                                                                       USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                           FILING DATE:
                                                                                                                                                                                        94608
                                                                                                                                               STATE: C
COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LENGTH:
```

```
(without alignments)
168.461 Million cell updates/sec
                                                                                                                      December 2, 2002, 10:00:50; Search time 2.17413 Seconds
GenCore version 5.1.3
Copyright (c) 1993 - 2002 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                               Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                              102317 seqs, 15924203 residues
                                                                                                                                                                                                                                     114
1 KTKRKKKQRVKIAYEEIFVKNM 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                OM protein - protein search, using sw model
                                                                                                                                                                                                                                                                                               BLOSUM62
Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                                                                                                                                                                                                                            Minimum DB seq length: 0
Maximum DB seq length: 2000000000
                                                                                                                                                                                                                US-09-741-106-10
                                                                                                                                                                                                                              Perfect score:
                                                                                                                                                                                                                                                                                               Scoring table:
                                                                                                                                                                                                                                                                                                                                                              Searched:
                                                                                                                                                                                                                                                    Sequence:
                                                                                                                         Run on:
```

/ Cgn2\_6/ptodata/1/pubpaa/USOB\_NBW\_PUB.pep:\*
/ Cgn2\_6/ptodata/1/pubpaa/USOB\_NBW\_PUB.pep:\*
/ Cgn2\_6/ptodata/1/pubpaa/USOG\_NBW\_PUB.pep:\*
/ Cgn2\_6/ptodata/1/pubpaa/USOG\_PUBCOMB.pep:\*
/ Cgn2\_6/ptodata/1/pubpaa/USOG\_PUBCOMB.pep:\*
/ Cgn2\_6/ptodata/1/pubpaa/USOZ\_PUBCOMB.pep:\*
/ Cgn2\_6/ptodata/1/pubpaa/USOZ\_NEW\_PUB.pep:\*
/ Cgn2\_6/ptodata/1/pubpaa/USOZ\_NEW\_PUB.pep:\*
/ Cgn2\_6/ptodata/1/pubpaa/USOZ\_NEW\_PUB.pep:\*

Published\_Applications\_AA:\*

Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Description	Sequence 3, Appli Sequence 1, Appli Sequence 1, Appli Sequence 1, Appli Sequence 1, Appli Sequence 11, Appli Sequence 22, Appli Sequence 22, Appli Sequence 22, Appli Sequence 226, Appli Sequence 41214, Appli Sequence 41214, Appli Sequence 177, Appli Sequence 177, Appli Sequence 177, Appli Sequence 171, Appli Sequence 171, Appli Sequence 1411, Appli
SUMMARIES	US-10-086-176A-3 US-10-086-176A-1 US-10-086-176A-1 US-10-086-176A-1 US-09-766-778-1 US-09-96-776-47012 US-09-90-529-714 US-09-907-537-2 US-09-907-537-2 US-09-907-537-2 US-09-905-291-714 US-09-986-761-41286 US-09-864-761-33591 US-09-864-761-33591 US-09-864-761-33591 US-09-915-242-5463 US-09-815-242-12164 US-09-815-242-12164
DB	000000000000000000000000000000000000000
% Query Match Length DB	23 30 430 50 50 60 60 60 60 60 60 60 60 60 6
% Query Match	100.0 100.0
Score	1114 1114 1114 1114 1114 1114 1114 111
Result No.	11111111111111111111111111111111111111

Sequence 47439, A			Sequence 45531, A	Sequence 156, App	Sequence 37061. A				Sequence 35536. A		_	Sequence 8. Appli	2	Segment 1 Appli	1 7	141	. ~							Segmence 8 Appli	· (7)
US-09-864-761-47439	US-09-864-761-40474	US-09-864-761-46109	US-09-864-761-45531	US-10-001-843-156	US-09-864-761-37061	US-09-864-761-36403	US-09-864-761-33832	US-09-864-761-34671	US-09-864-761-35536	US-09-864-761-36893	US-09-925-299-841	US-09-938-803-8	: US-10-015-498-2	US-09-978-242-1	US-09-821-687-4	US-09-925-300-1415	US-09-828-423-4	US-09-925-301-1335	US-09-815-242-10439	US-09-815-242-14042	US-09-925-300-1099	US-09-864-761-35548	US-09-812-133-2	US-09-813-398-8	US-09-349-954A-22
25 10	47 10	52 10	54 10	67 12	71 10	85 10	86 10	86 10	130 10	141 10	216 10	241 10	361 12	545 10	561 10	579 10	911 10	1005 10	1407 10	1407 10	37 10	72 10	171 10	190 9	214 10
35.1	35.1	35.1	35.1	35.1	35.1	35.1	35.1	35.1	35.1	35.1	35.1	35.1	35.1	35.1	35.1	35.1	35.1	35.1	35.1	35.1	34.2	34.2	34.2	34.2	34.2
40	40	40	40	40	40	40	40	40	40	40	40	40	40	40	40	40	40	40	40	40	39	39	39	39	39
20	21	22	23	24	25	56	27	28	58	30	31	32	33	34	32	36	37	38	39	40	41	42	43	44	45

## ALIGNMENTS

; Sequence 3, Application US/10086176A ; Patent No. US20020173465A1

RESULT 1 US-10-086-176A-3

```
GENERAL INCOMMATION:
APPLICANT: Hembrough, Todd
APPLICANT: Papathanassiu, Adonia E.
APPLICANT: Papathanassiu, Abonia E.
APPLICANT: Papathanassiu, Abban J.
ITILE OF INVENTION: Compositions and Methods for Inhibiting Cellular Proliferation
ITILE OF INVENTION: TFPI Fragments
ITILE OF INVENTION: TPPI Fragments
ITILE OF INVENTION: TPPI Fragments
ITILE OF INVENTION: 1891-0296
CURRENT FILING DATE: 2002-02-28
FRIOR APPLICATION NUMBER: US 09/766,778
PRIOR APPLICATION NUMBER: US 09/227,955
PRIOR PRILING DATE: 1999-01-11
PRIOR PILING DATE: 1999-01-11
PRIOR APPLICATION NUMBER: US 08/796,850
PRIOR PILING DATE: 1997-02-06
PRIOR APPLICATION NUMBER: US 09/130,273
PRIOR FILING DATE: 1998-06-06
NUMBER OF SEQ ID NOS: 6
SOFTWARE: PatentIn version 3.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       .;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 23;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            100.0%; Score 114; DB 9;
100.0%; Pred. No. 9.1e-10;
tive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; OTHER INFORMATION: Synthetic peptide US-10-086-176A-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 KTKKKKKKQRVKIAYEEIFVKNM 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity 100.0
Matches 23; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQ ID NO 3
LENGTH: 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            q
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              δ
```

RESULT 2 US-10-086-176A-2

```
APPLICANT: Hembrough, Todd
APPLICANT: Papathanassiu, Adonia E.
APPLICANT: Green, Shawn J.
TITLE OF INVENTION: Compositions and Methods for Inhibiting Cellular Proliferation
TITLE OF INVENTION: Compositions and Methods for Inhibiting Cellular Proliferation
TITLE OF INVENTION: TFPI Fragments
FILE REFERENCE: 05213-0296 43170-266780
CURRENT APPLICATION NUMBER: US/10/086,176A
PRIOR APPLICATION NUMBER: US 09/766,778
PRIOR APPLICATION NUMBER: US 09/727,955
PRIOR PELING DATE: 1999-01-11
PRIOR FILING DATE: 1999-01-12
PRIOR FILING DATE: 1999-01-306/850
PRIOR FILING DATE: 1999-01-306/850
PRIOR PELING DATE: US 08/730,273
PRIOR APPLICATION NUMBER: US 09/130,273
PRIOR APPLICATION NUMBER: US 09/130,273
PRIOR APPLICATION NUMBER: US 09/130,273
PRIOR PELLING DATE: 1999-01-66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TITLE OF INVENTION: Compositions and Methods for Inhibiting Cellular Proliferation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 276;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ADDRESSEE: Jones & Askew
STREET: 191 Peachtree Street, 37th Floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           100.0%; Score 114; DB 9;
nilarity 100.0%; Pred. No. 1.2e-08;
Conservative 0; Mismatches n.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: US/09/766,778
FILING DATE: 22-Jan-2001
CLASSIFICATION: <UNKNOWN>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: 09/227,955
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Papathanassiu, Adonia E
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; OTHER INFORMATION: Synthetic peptide US-10-086-176A-5
                                                                                                                                                                                      Sequence 5, Application US/10086176A; Patent No. US20020173465A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          254 KTKRKKKKQRVKIAYEEIFVKNM 276
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; Sequence 1, Application US/09766778 ; Patent No. US20010018204A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 KTKRKKKÇRVKIAYEEIFVKNM 23
1 KTKRKKKKQRVKIAYEEIFVKNM 23
                            23 KTKRKKKQRVKIAYEEIFVKNM 45
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Shawn J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NUMBER OF SEQ ID NOS: 6
SOFTWARE: PatentIn version 3.1
SEQ ID NO 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STATE: Georgia
COUNTRY: U.S.A.
ZIP: 30303
COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CITY: Atlanta
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity
Matches 23; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GENERAL INFORMATION:
                                                                                                                                                                    US-10-086-176A-5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LENGTH: 276
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 5
US-09-766-778-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   : PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  δλ
                                              qq
     οy
                                                                                                  APPLICANT: Hemilal Lowyll, 1004

APPLICANT: Papathanassiu, Adonia E.
APPLICANT: Green, Shawn J.
TITLE OF INVENTION: Compositions and Methods for Inhibiting Cellular Proliferation CC
TITLE OF INVENTION: TEPI Fragments
FILE REFERENCE: 05213-0296 43170-266780
CURRENT PILLICATION NUMBER: US/10/086,176A
CURRENT FILING DATE: 2002-02-28
PRIOR PLICATION NUMBER: US 09/766,778
PRIOR PLICATION NUMBER: US 09/727,955
PRIOR FILING DATE: 1999-01-11
PRIOR APPLICATION NUMBER: US 08/729,855
PRIOR FILING DATE: 1999-02-06
PRIOR PLICATION NUMBER: US 09/130,273
PRIOR PLICATION NUMBER: US 09/130,273
PRIOR PLING DATE: 1999-02-06
PRIOR PLING DATE: 1999-02-06
PRIOR PLING DATE: 1999-03-06
SOFTWARE: PATENTING DATE: US 08/130,273
PRIOR PLING DATE: US 08/130,273
PRIOR FILING DATE: US 08/130,273
PRIOR FILING DATE: US 08/130,273
PRIOR FILING DATE: US 08/130,273
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GENERAL INFORMATION:

APPLICANT: Hembrough, Todd

APPLICANT: Hembrough, Todd

APPLICANT: Hembrough, Todd

APPLICANT: Green, Shawn J.

TITLE OF INVENTION: Compositions and Methods for Inhibiting Cellular Proliferation CG

TITLE OF INVENTION: TFPI Fragments

FILE REPERENCE: 05213-0296 43170-266780

CURRENT APPLICATION NUMBER: US/10/086,176A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ch 100.0%; Score 114; DB 9; Length 45; 1 Similarity 100.0%; Pred. No. 1.8e-09; 23; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 30;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 100.0%; Score 114; DB 9; Best Local Similarity 100.0%; Pred. No. 1.2e-09; Matches 23; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CURRENT FILING DATE: 2002-02-28
PRIOR APPLICATION NUMBER: US 09/766,778
PRIOR PILING DATE: 2001-01-22
PRIOR PELLING DATE: 1999-01-11
PRIOR FILING DATE: 1999-01-11
PRIOR PILING DATE: 1999-01-11
PRIOR PILING DATE: 1999-01-13
PRIOR PILING DATE: 1999-01-05
PRIOR PILING DATE: 1998-06
NUMBER OF SEQ ID NOS: 6
SOGTWARE: PATENTIN VERSION 3.1
SEQ ID NO 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CTHER INFORMATION: Synthetic peptide US-10-086-176A-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; OTHER INFORMATION: Synthetic peptide US-10-086-176A-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 1, Application US/10086176A Patent No. US20020173465A1
     Sequence 2, Application US/10086176A Patent No. US20020173465A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            8 KTKRKKKQRVKIAYEEIFVKNM 30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 KTKRKKKKQRVKIAYEEIFVKNM 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ORGANISM: Artificial Sequence
                                                            GENERAL INFORMATION:
APPLICANT: Hembrough, Todd
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT 3
US-10-086-176A-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                g
```

FILING DATE: <Unknown>

```
Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; Sequence 714, Application US/09925297; Patent No. US20020081659A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    43.98;
64.38;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity 64.33,
Post Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         3 KRKRKKQRVKIAYE 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             25 KRPRKAQRLRVAYE 38
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT 7
US-09-925-297-714
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQ ID NO 47012
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           рp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ó:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LOCATION: 167..168
OTHER INFORMATION: /note= "Potential site for N-linked
glycosylation"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                LOCATION: 117..118
OTHER INFORMATION: /note= "Potential site for N-linked
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LOCATION: 228.229
OTHER INFORMATION: /note= "Potential site for N-linked
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 276;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
                                                                                                                                                                                                                                                                                                                                                                          LOCATION: 2..3
OTHER INFORMATION: /note= "Site of partial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 100.0%; Score 114; DB 10; Best Local Similarity 100.0%; Pred. No. 1.2e-08; Matches 23; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; SEQUENCE DESCRIPTION: SEQ ID NO: 1: US-09-766-778-1
               NAME: Greene, Jamie L.
REGISTRATION NUMBER: 32,467
REFERENCE/DOCKET NUMBER: 05213-0290
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /label= Kunitz-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LOCATION: 97..147
OTHER INFORMATION: /label= Kunitz-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 47012, Application US/09864761
Patent No. US20020048763A1
GENERAL INFORMATION:
                                                               TELECOMMUNICATION INFORMATION:
TELEPHONE: (404) 818-3700
TELEFAX: (404) 818-3799
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                         LENGTH: 276 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME/KEY: Active-site
LOCATION: 228..229
                                                                                                                                                                            TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME/KEY: Active-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME/KEY: Active-site
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                         ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                           NAME/KEY: Active-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 KTKRKKKQRVKIAYEEIFVKNM 23
                                                                                                                                                                                                                                                                 ANTI-SENSE: NO
FRAGMENT TYPE: N-terminal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LOCATION: 189..239 OTHER INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LOCATION: 26..76
OTHER INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME/KEY: Domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME/KEY: Domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME/KEY: Domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Penn, Sharron G. APPLICANT: Rank, David R. APPLICANT: Hanzel, David K.
                                                                                                                                                                                                                                                                                                                                                                                                               phosphorylation"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Chen, Wensheng
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     glycosylation"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      glycosylation"
                                                                                                                                                                                                                                                                                                      ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US-09-864-761-47012
                                                                                                                                                                                                                                                                                                                                        FEATURE
                                                                                                                                                                                                                                                                                                                                                                                                                                FEATURE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FEATURE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FEATURE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FEATURE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FEATURE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FEATURE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 õ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               qq
```

```
TITLE OF INVENTION: GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FO TILLE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY CURRENT APPLICATION NUMBER: US-02/99/864,761
CURRENT APPLICATION NUMBER: US-02/99/864,761
PRIOR APPLICATION NUMBER: US-02/90/964,761
PRIOR PILING DATE: 2000-09-26
PRIOR PAPLICATION NUMBER: US-02/90/964
PRIOR PAPLICATION NUMBER: US-02/90/964
PRIOR APPLICATION NUMBER: US-02/90/964
PRIOR PAPLICATION NUMBER: US-02/90/966
PRIOR PAPLICATION NUMBER: US-02/90/966
PRIOR PAPLICATION NUMBER: PS-02/90/966
PRIOR PAPLICATION NUMBER: PS-02/90/90/97
PRIOR PILING DATE: 2001-01-30
PRIOR PILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CTHER INFORMATION: MAP TO AC005600.1
OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 0.54
OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 0.45
OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 0.41
OTHER INFORMATION: EXPRESSED IN AB53883.1, EVALUE 2.00e-51
US-09-864-761-47012
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 50; DB 10; Length 95;
Pred. No. 1.5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GENERAL INFORMATION:
APPLICANT: Rosen et al.
TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
FILE REFERENCE: PA105
```

```
APPLICANT: Al-Garawi, Amal APPLICANT: Al-Garawi, Amal APPLICANT: Miller, Charles APPLICANT: Tomb, Jean Francois APPLICANT: Tomb, Jean Francois APPLICANT: Tomb, Jean Francois APPLICANT: Oomen, Raymond P. TITLE OF INVENTION: Identification of Polynucleotides TITLE OF INVENTION: Encoding No. US20020160456Alel Helicobacter Polypeptides in tTITLE OF INVENTION: Genome FILE REFERENCE: 06132/043002 CURRENT PAPLICATION NUMBER: US/09/895,913A CURRENT FILING DATE: 2001-06-29 PRIOR APPLICATION NUMBER: US 08/881,227 PRIOR FILING DATE: 1997-06-24 SOUTHWARE OF SEQ ID NOS: 368 SOFTWARE: FastSEQ for Mindows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Penn, Sharron G.
APPLICANT: Penn, David R.
APPLICANT: Penn, David R.
APPLICANT: Chen, Wensheng
TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FO
TITLE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY
FILE REFERENCE: Accomica-X-1
CURRENT APPLICATION NUMBER: US/09/864,761
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ő
                                                                                                                                                          ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                            Gaps
                                                                                                                                                          ó;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 42; DB 9; Length 999;
Pred. No. 2e+02;
6; Mismatches 3; Indels
                                                                                                      Score 42; DB 9; Length 76; Pred. No. 14; 2; Indels 1; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CURRENT FILING DATE: 2001-05-23

PRIOR FILING DATE: 2000-05-3

PRIOR FILING DATE: 2000-05-04

PRIOR FILING DATE: 2000-05-05

PRIOR PLICATION NUMBER: US 60/207,456

PRIOR FILING DATE: 2000-05-26

PRIOR FILING DATE: 2000-08-03

PRIOR FILING DATE: 2000-08-03

PRIOR PLICATION NUMBER: US 60/23,566

PRIOR PLICATION NUMBER: US 09/632,967

PRIOR APPLICATION NUMBER: US 60/236,59

PRIOR PLING DATE: 2000-08-03

PRIOR PLING DATE: 2000-09-27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 41214, Application US/09864761 Patent No. US20020048763A1
                                                                                                                                                                                                                                                                                                                                                                     Sequence 226, Application US/09895913A

Patent No. US20020160456A1

; GENERAL INFORMATION:

APPLICANT: Kleanthous, Harold
                                                                                                              36.8%;
75.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ORGANISM: Helicobacter pylori
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         36.8%;
43.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Ouery Match
Best Local Similarity 43...
7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               :||:|:|: |: |: 346 ERKKKRQKSKLALNEL 361
                                                                                                              Query Match
Best Local Similarity 75.0
Matches 9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 3 KRKRKKQRVKIAYEEI 18
                                                                                                                                                                                                                                      TYPE: PRT
ORGANISM: Homo sapien
                                                                                                                                                                                                             1 KTKKKKKKRVK 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-09-864-761-41214
                                                                                                                                                                                                                                                                                                                              RESULT 10
US-09-895-913A-226
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-09-895-913A-226
                                                                    US-10-002-344A-229
LENGIH: 76
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         δλ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Sun, Yongming
APPLICANT: Chen, Sel-Yu
APPLICANT: Liu, Chenghua
APPLICANT: Liu, Chenghua
TITLE OF INVENTION: Compositions and Methods Relating to Lung Specific Genes and Prot
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ij
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           3,
                                                                                                                                                                                                                                                                                                                                                                               7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 357;
                                                                                                                                                                                                                                                                                                                                     DB 10; Length 201;
                                                                                                                                                                                                                                                                                                                                                                               Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GENERAL INFORMATION:
APPLICANT: Meyers, Rachel
APPLICANT: Tsai, Fong-Ying
TITLE OF INVENTION: 42755, A NOVEL HUMAN METHYLTRANSFERASE
TITLE OF INVENTION: FAMILY MEMBER AND USES THEREOF
FILE REPERENCE: MNI-176
CURRENT APPLICATION NUMBER: US/09/907,537
CURRENT ELING DATE: 2001-07-16
PRIOR APPLICATION NUMBER: 60/218,470
PRIOR FILING DATE: 2000-07-14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            37.3%; Score 42.5; DB 10; 50.0%; Pred. No. 60;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           9:
                                                                                                                                                                                                                                                                                                                                   37.3%; Score 42.5; D 43.5%; Pred. No. 33; tive 4; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FILE REFERENCE: DEX-0241
CURRENT APPLICATION NUMBER: US/10/002,344A
CURRENT FILING DATE: 2002-03-15
PRIOR APPLICATION NUMBER: US 60/242,998
PRIOR FILING DATE: 2000-10-25
                   CURRENT FILING DATE: 2001-08-10
PRIOR APPLICATION NUMBER: PCT/US00/05989
PRIOR FILING DATE: 2000-03-08
PRIOR FILING DATE: 1999-03-12
NUMBER OF SEQ ID NOS: 928
SOFTWARE: PATENTIN VET. 2.0
SEQ ID NO 714
LENGTH: 201
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NUMBER OF SEQ ID NOS: 3
SOFWTARE: FastSEQ for Windows Version 4.0
SEQ ID NO 2
LENGTH: 357
    CURRENT APPLICATION NUMBER: US/09/925,297
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 229, Application US/10002344A patent No. US20020172999A1 GENERAL INFORMATION: APPLICANT: Recipon, Herve
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 2, Application US/09907537 Patent No. US20020068348A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 KTKRKRK-----KQRVKIAYE 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 KTKRKKKQRVKIAYEEIFVKN 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NUMBER OF SEQ ID NOS: 277
SOFTWARE: PatentIn version 3.1
SEQ ID NO 229
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Ouery Match 37.3°
Best Local Similarity 50.0°
Matches 11; Conservative
                                                                                                                                                                                                                                                                                                                                                         Best Local Similarity 43.5
Matches 10; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; ORGANISM: Homo sapiens US-09-907-537-2
                                                                                                                                                                                                                                      TYPE: PRT
CORGANISM: Homo sapiens
US-09-925-297-714
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 9
US-10-002-344A-229
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT 8
US-09-907-537-2
                                                                                                                                                                                                                                                                                                                                     Query Match
```

qq ð

```
Sequence 177, Application US/09764846
Patent No. US20020102638A1
Jeneral No. US20020102638A1
Jeneral No. US20020102638A1
JENERAL TOO:
TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
FILE REFERENCE: PT212
CURRENT FILING DATE: 2001-01-17
Prior application data removed - consult PALM or file wrapper
NUMBER OF SEQ ID NOS: 348
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 177
LENGTH: 63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 41; DB 10; Length 57;
Pred. No. 14;
3; Mismatches 5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 1.4
OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 1.5
OTHER INFORMATION: EXPRESSED IN ADDLT LIVER, SIGNAL = 1.4
OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 1.2
OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 1.2
OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 1.2
OTHER INFORMATION: EXPRESSED IN HEARY, SIGNAL = 1.3
                                 FRIOR APPLICATION NUMBER: US 60/236,359
PRIOR FILING DATE: 2000-09-27
PRIOR PELING DATE: 2000-09-27
PRIOR APPLICATION NUMBER: PCT/US01/00666
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00664
PRIOR FILING DATE: 2001-01-30
PRIOR PELING DATE: 2001-01-30
PRIOR FILING DATE: 2001-01-30
PRIOR PELING DATE: 2001-01-30
PRIOR FILING DATE: 2001-01-30
PRIOR PELING DATE: 2001-01-30
PRIOR FILING DATE: 2001-01-30
PRIOR FILING DATE: 2001-01-30
PRIOR FILING DATE: 2000-09-21
PRIOR FILING DATE: 2000-09-31
PRIOR FILING DATE: 2001-01-30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 OTHER INFORMATION: MAP TO AL157381.7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  36.0%;
52.9%;
                         FILING DATE: 2000-10-04
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 KTKKKKKQRVKIAYEE 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    | |||:||:: | ||
| KRKRKKKKKKKKEEE 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Best Local Similarity 52.9
Matches 9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-09-864-761-41286
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 13
US-09-764-846-177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-09-764-846-177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Penn, Sharron G.
APPLICANT: Penn, Sharron G.
APPLICANT: Rank, David R.
APPLICANT: Hanzel, David K.
APPLICANT: Honzel, David K.
APPLICANT: Chen, Wensheng
TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR PILLE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY
FILE REFERENCE: Aeomica-X-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB 10; Length 56;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 1.8
OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 1.3
OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 1.6
OTHER INFORMATION: EXPRESSED IN PETAL LIVER, SIGNAL = 1.3
OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 1.1
OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 1.4
OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 1.4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                5; Indels
            PRIOR APPLICATION NUMBER: PCT/USO1/00666

PRIOR FILING DATE: 2001-01-30

PRIOR FILING DATE: 2001-01-30

PRIOR FILING DATE: 2001-01-30

PRIOR PRIOR POTICATION NUMBER: PCT/US01/00664

PRIOR APPLICATION NUMBER: PCT/US01/00669

PRIOR PILING DATE: 2001-01-30

PRIOR PLING DATE: 2001-01-30

PRIOR FILING DATE: 2001-01-30

PRIOR FILING DATE: 2001-01-30

PRIOR PLING DATE: 2001-01-30

PRIOR APPLICATION NUMBER: PCT/US01/00668

PRIOR APPLICATION NUMBER: PCT/US01/00668

PRIOR PLING DATE: 2001-01-30

PRIOR APPLICATION NUMBER: PCT/US01/00661

PRIOR APPLICATION NUMBER: PCT/US01/00670

PRIOR APPLICATION NUMBER: US 00/234,687

PRIOR PLING DATE: 2001-01-30

PRIOR PLING DATE: 2001-01-30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 41; DB 1
Pred. No. 14;
3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CURRENT FILING DATE: 2001-05-23
PRIOR APPLICATION NUMBER: US 60/180,312
PRIOR FILING DATE: 2000-02-04
PRIOR APPLICATION NUMBER: US 60/207,456
PRIOR FILING DATE: 2000-05-26
PRIOR FILING DATE: 2000-06-38
PRIOR FILING DATE: 2000-08-03
PRIOR APPLICATION NUMBER: US 69/632,366
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CURRENT APPLICATION NUMBER: US/09/864,761
    APPLICATION NUMBER: PCT/US01/00666
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 41286, Application US/09864761
Patent No. US20020048763A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       OTHER INFORMATION: MAP TO AC009311.2 OTHER INFORMATION: EXPRESSED IN LUNG,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 36.0%;
52.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 KTKRKKKKQRVKIAYEE 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-09-864-761-41214
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-09-864-761-41286
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FEATURE:
PRIOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   q
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           δ
```

Gaps

.; 0

g δ

```
APPLICANT: Hanzel, David K.
APPLICANT: Chen, Wensheng
TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FO TITLE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY
FILE REFERENCE: Acomica-X-1
CURRENT APPLICATION NUMBER: US/09/864,761
CURRENT FILING DATE: 2001-05-23
                                                                                                                                                                                                                                                                                                           ;
0
                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                           ;
                                                                                                                                                                                                                                  36.0%; Score 41; DB 10; Length 89; 52.9%; Pred. No. 23; Live 3; Mismatches 5; Indels
IN PLACENTA, SIGNAL = 2.7
IN HELA, SIGNAL = 2.1
IN BONE MARROW, SIGNAL = 2.4
IN BH474, SIGNAL = 1.3
IN HBL100, SIGNAL = 1.7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Annomax Sequence Listing Engine vers. 1.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRIOR PELLANG DATE: 2001-03-23
PRIOR FILING DATE: 2000-02-04
PRIOR PELLING DATE: 2000-05-26
PRIOR PELLING DATE: 2000-05-26
PRIOR PELLING DATE: 2000-05-26
PRIOR PELLING DATE: 2000-05-26
PRIOR PELLING DATE: 2000-06-33
PRIOR PELLING DATE: 2000-09-37
PRIOR PELLING DATE: 2000-09-37
PRIOR PELLING DATE: 2000-09-37
PRIOR PELLOATION NUMBER: GB 24263, 359
PRIOR PELLING DATE: 2001-01-30
PRIOR PELLING DATE: 2000-09-21
PRIOR PELLING DATE: 2000-09-21
PRIOR PELLING DATE: 2000-09-30
PRIOR PELLING DATE: 2000-09-30
PRIOR PELLING DATE: 2000-09-30
PRIOR PELLOATION NUMBER: US 60/234,687
PRIOR PELLING DATE: 2000-09-30
PRIOR PELLING DATE: 2000-09-30
PRIOR PELLING DATE: 2000-09-30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; Sequence 33599, Application US/09864761; Patent No. US20020048763A1
                                      EXPRESSED
EXPRESSED
EXPRESSED
EXPRESSED
          EXPRESSED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GENERAL INFORMATION:
APPLICANT: Penn, Sharron G.
APPLICANT: Rank, David R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NUMBER OF SEQ ID NOS: 49117
                                                                                                                                                                                                                                                                                                                                                                             1 KTKKKKKKQRVKIAYEE 17
                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 36.0°
Best Local Similarity 52.9°
Matches 9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: PRT ORGANISM: Homo sapiens FEATURE:
      ; OTHER INFORMATION: E
US-09-864-761-35241
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-09-864-761-33599
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQ ID NO 33599
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LENGIH: 101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SOFTWARE:
                                                                                                                                                                                                                                                                                                                                                                                                                                               Db
                                                                                                                                                                                                                                                                                                                                                                                       δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Penn, Sharron G.
APPLICANT: Rank, David R.
APPLICANT: Hanzel, David K.
APPLICANT: Chen, Wensheng
TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
TITLE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY
                                                                                                               0;
                                                                                                                      Gaps
                                                                                                                  ;
                                         Length 63;
                                                                                                               2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 3
OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 1.4
OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 2.1
OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 3.0
OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SOFTWARE: Annomax Sequence Listing Engine vers. 1.1
                                             Score 41; DB 10;
Pred. No. 16;
                                                                                                                      6; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         THILE OF LINGENITOR.

CURRENT APPLICATION NUMBER: US/09/864,761

CURRENT FILING DATE: 2001-05-23

PRIOR PELICATION NUMBER: US/09/864,761

PRIOR PELICATION NUMBER: US 60/180,312

PRIOR PELICATION NUMBER: US 60/207,456

PRIOR PLILING DATE: 2000-05-26

PRIOR PELICATION NUMBER: US 60/207,456

PRIOR PELICATION NUMBER: US 60/207,456

PRIOR PELICATION NUMBER: US 60/23,366

PRIOR PELICATION NUMBER: US 60/236,359

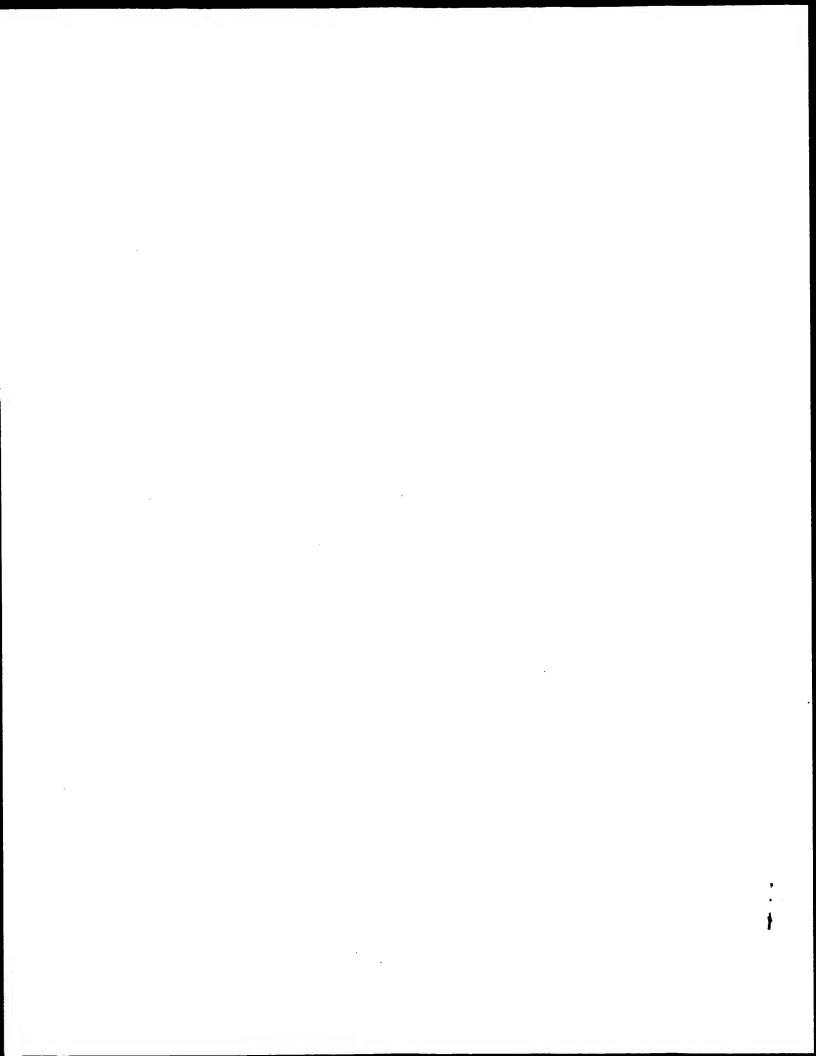
PRIOR PELICATION NUMBER: US 60/236,359

PRIOR PELING DATE: 2000-09-27

PRIOR PELING DATE: 2001-01-30

PRIOR PILING DATE: 2001-01-30

PRIOR PELING DATE: 2001-01-30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRIOR APPLICATION NUMBER: US 09/774,203
PRIOR FILLING DATE: 2001-01-29
NUMBER OF SEQ ID NOS: 49117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 OTHER INFORMATION: MAP TO AL034548.24
                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 35241, Application US/09864761 Patent No. US20020048763A1
                                                    36.0%;
46.7%;
                 Query Match
Best Local Similarity 46./.
7; Conservative
                                                                                                                                                                                 1 KTKRKKKKQRVKIAY 15
                                                                                                                                                                                                                              48 KKKKKKKKKKKISW 62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                       US-09-864-761-35241
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQ ID NO 35241
LENGTH: 89
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FEATURE:
```



```
GenCore version 5.1.3
Copyright (c) 1993 - 2002 Compugen Ltd.
```

OM protein - protein search, using sw model

December 2, 2002, 10:00:35 ; Search time 4.1194 Seconds Run on:

(without alignments) 536.751 Million cell updates/sec

US-09-741-106-10 Perfect score:

1 KTKRKKKÇRVKIAYEEIFVKNM 23 Sequence:

Scoring table:

BLOSUM62 Gapop 10.0 , Gapext 0.5

Total number of hits satisfying chosen parameters:

283224 seqs, 96134422 residues

Searched:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

PIR\_73:\* Database

1: pir1:\* 2: pir2:\* 3: pir3:\* 4: pir4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

		æ			SUMMAKIES	
Result	Č	Query				
. ON .	score	Match	Match Length	BB :	ID	Description
<b>.</b>	114	100.0	304	Н	TIHUGK	tissue factor path
7	113		304	Н	JC2264	factor
co	91	٠	396	N	S53325	factor
4	77		299	~	146937	factor
2	77	67.5	300	~	121	otein-as
9	26		272	7	T01480	_
7	52	٠	4981	7	T18489	
œ	49		114	7	C97205	N
6	49		298	7	G90529	heat shock protein
10	4		357	7	G69393	conserved hypothet
11	48.5	42.5	135	7	T38956	very hypothetical
12	48	42.1	231	~	T48215	translation initia
13	48	42.1	727	N	T26096	hypothetical profe
14	₹*	42.1	2025	~	JC5020	tetratricopentide
15	47.5	41.7	182	~	AC0545	hypothetical profe
16	47	41.2	780	N	G72405	ATP-dependent DNA
17	47	41.2	1113	7	T20004	hypothetical profe
18	47	41.2	1633	7	JC5056	polybromo 1 - chic
19	9	40.8	310	~	A33489	Ω
20	9	40.8	402	7	T45518	
21	9	40.8	402	7	AC2304	Ø
22	9	40.8	402	7	AC2552	Ø
23	9	40.8	402	7	AD2506	
24	9	40.8	402	~	AG2506	
25	9	40.8	402	7	AI2318	
56	46.5	40.8	413	~	AG2456	
27	46.5	40.8	653	7	F70383	
28	46	40.4	240	~	H72294	
29	45	39.5	402	7	S47329	

transcription init genome polyprotein prohable alvoice.t	hypothetical prote RNA polymerase sig	spore coat protein proximal sequence hypothetical prote	hypothetical prote hypothetical prote	splicing factor Pr transposase all715 translation initia	hypothetical prote hypothetical prote	
S78176 RRXPLC S48285	A97110 G83851	69/25/ JC6081 G86181	C59097 H71609	F30109 AF2497 T04935	T49173 C83652	T23500
212	000	700	222	7 7 7	2 2	7
532 2210 667	126	368 413	492 1166	407 471	517 317	342
39.5	38.6	38.0	38.6	3886	38.2	37.7
45 45 44.5	4 4 4	* † † † † †	444	43.5 43.5	43.5	43
30 31 32	333 1433	36 37	8 6 C	4 4 1 2 2	43	45

### ALIGNMENTS

Н	
ULT	
SG	7111
ΕĀ	ŀ

tissue factor pathway inhibitor precursor [validated] - human
NAlternate names: extrinsic pathway inhibitor; lipoprotein-associated coagulation in
C;Species: Homo sapiens (man)
C;Date: 30-Jun-1992 #sequence\_revision 30-Jun-1992 #text\_change 08-Dec-2000
C;Date: 30-Jun-1992 #sequence\_revision 30-Jun-1992 #text\_change 08-Dec-2000
C;Accession: A53712; A39176; A28650; A60433; B60433; S13034; A34315; A38294; S03903
C;Accession: A57372; Wesselschmidt, R.L.; MacPhail, L.A.; Likert, K.M.; Byers, M.J. Biol. Chem. 266, 5036-5041, 1991
A;Title: Structure of the human lipoprotein-associated coagulation inhibitor gene. In
A;Reference number: A23712; MUID:91161593; PMID:2002045

A; Molecule type: DNA

A; Residues: 1-304 <GIR>

A)Cross-references: GB:M59493; GB:M59499; NID:9187204; PIDN:AAA59526.1; PID:9187206
R; van der Logt, C.P.E.; Reitsma, P.H.; Bertina, R.M.
Biochemistry 30, 1571-1577, 1991
A;Title: Intron-exon organization of the human gene coding for the lipoprotein-associ
A; Reference number: A39176; MUID:91129227; PMID:1993173

A; Molecule type: DNA A; Residues: 1-304 <VAN>

A)Cross-references: GB:M58650; GB:J05312; NID:9186827; PIDN:AAA59480.1; PID:9186829 R;Wun, T.C.; Kretzmer, K.K.; Girard, T.J.; Miletich, J.P.; Broze Jr., G.J. J. Blol. Chem. 263, 6001-6004, 1988 A;Title: Cloning and characterization of a cDNA coding for the lipoprotein-associated A;Reference number: A28650; MUID:88198127; PMID:2452157

A; Molecule type: mRNA A; Residues: 1-304 <WUN>

A.Cross references: GB.J03225; NID:g180545; PIDN:AAA52022.1; PID:g180546
A.Note: part of this sequence, including the amino end of the mature protein, was con forgard, T.J.; Warren, L.A.; Novotny, W.F.; Bejcek, B.E.; Miletich, J.P.; Broze Jr., Thromb. Res. 55, 37-50, 1989
A.Title: Identification of the 1.4 KB and 4.0 KB messages for the lipoprotein associa A.Reference number: A60433; MUID:89388722; PMID:2781520
A.Status: not compared with conceptual translation

A; Molecule type: mRNA A; Residues: 1-304 <GI

A; Experimental source: endothelial cells L-304 <GI2>

A; Accession: B60433

A; Molecule type: protein
A;Residues: 'XX',31-53,'X',55-56 <G13>
A;Residues: 'XX',31-53,'X',55-56 <G13>
A;Residues: 'XX',31-53,'X',55-56 <G13>
B;Breard, T.J.; McCourt, D.; Novotny, W.F.; MacPhail, L.A.; Likert, K.M.; Broze Jr., Biochem. J. 270, 621-625, 1990
A;Title: Endogenous phosphorylation of the lipoprotein-associated coagulation inhibit A;Reference number: S13034; MUID:91054349; PMID:2122883

A; Molecule type: protein A; Residues: 29-35 <GI4>

```
374 KTKRKKKQTVKIVYEKIFVKKL 396
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     282 KTKRKRKKQRVKIAYEEVFVKNM 304
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 KTKKKKKKQRVKIAYEEIFVKNM 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 KTKKKKKQRVKIAYEEIFVKNM 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 KTKKKKKKKORVKIAYEEIFVK 21
                                                                                                                                                                                                                                                                                                                                                                                             99.18;
95.78;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         78.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Best Local Similarity 78.3
Matches 18; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                         Local Similarity
Les 22; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Molecule type: mRNA
A: Residues: 1-299 <BEL>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                q
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              δλ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          δλ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               UC2264

JUC2264

JUC2264

JUC2264

JUC2264

JUL15sue factor pathway inhibitor precursor - rhesus macaque
N.Alternate names: extrinsic pathway inhibitor; lipoprotein-associated coagulation inhib
C; Species: Macaca mulatta (rhesus macaque)
C; Date: 10.5ep-1999 #sequence_revision 10-Sep-1999 #text_change 21-Jul-2000
C; Accession: JUC2264
R; Kamel, S.; Kamikubo, Y.; Hamuro, T.; Fujimoto, H.; Ishihara, M.; Yonemura, H.; Miyamot
J; Biochem. 115, 708-714, 1994
A; Title: Amino acid sequence and inhibitory activity of rhesus monkey tissue factor path
A; Reference number: JUC264
A; MID:94375417; PMID:8089087
A; Maccession: JUC264
A; MUD:94375417; PMID:8089087
A; Molecule type: mRNA
A; Residues: 1-304
A; Multiple minibitor the activities of factor Xa and tissue factor-factor VI
C; Comment: This protein inhibits the activities of factor Xa and tissue factor-factor VI
C; Comment: This protein inhibits the activities of factor xa and tissue factor-factor VI
C; Superfamily: tissue factor pathway inhibitor; animal Kunitz-type proteinase inhibitor
C; Reywords: anticoagulant; glycoprotein; serine proteinase inhibitor
F; 1-28/Domain: adjund sequence #status predicted <SIG>
R:Novotny, W.F.; Girard, T.J.; Miletich, J.P.; Broze Jr., G.J.
J. Biol. Chem. 264, 18932-1893
A. Title: Purification and characterization of the lipoprotein-associated coagulation inl.
A. Accession. A34315
A. Accession. A34316
A. Accession. A3416
A. Accession. A3417
A. Accession. Accession. Aaccession. Aaccession. Aaccession. Aaccession. Aacc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         F:135/Inhibitory site: Arg (coagulation factor X) #status experimental F:145,195,256/Binding site: carbohydrate (Asn) (covalent) #status predicted F:227/Inhibitory site: Arg (unidentified proteinase) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 304;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         100.0%; Score 114; DB 1;
100.0%; Pred. No. 1.9e-08;
tive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        282 KTKRKRKKQRVKIAYEEIFVKNM 304
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 KTKRKKKKQRVKIAYEEIFVKNM 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       23;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       q
```

```
Spains factor pathway inhibitor - rabbit
C;Species: Oryctolagus cuniculus (domestic rabbit)
C;Species: Oryctolagus cuniculus (domestic rabbit)
C;Date: Ol-Aug-1995 #sequence_revision 01-Sep-1995 #text_change 16-Jul-1999
C;Accession: S53325
R;Girard, T.J.; Gallani, D.; Broze Jr., G.J.
Biochem. J. 303, 923-928, 1994
A;Title: Complementary DNA sequencing of canine tissue factor pathway inhibitor revea
A;Reference number: S53325
A;Accession: S53325
A;Accession: S53325
A;Accession: S53325
A;Residues: prellminary
A;Molecule type: mRNA
A;Molecule type: mRNA
A;Molecule type: mRNA
C;Superfamily: animal Kunitz-type proteinase inhibitor homology
C;Keywords: serine proteinase inhibitor homology RPD>
F;3103-105/Domain: animal Kunitz-type proteinase inhibitor homology SPD>
F;309-359/Domain: animal Kunitz-type proteinase inhibitor homology RPD>
F;309-359/Domain: animal Kunitz-type proteinase inhib
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Cross-references: GB:S61902; NID:9386015; PIDN:AAB26836.1; PID:9386016
C;Superfamily: tissue factor pathway inhibitor; animal Kunitz-type proteinase inhibit F;49-99/Domain: animal Kunitz-type proteinase inhibitor homology <BPII>F;120-170/Domain: animal Kunitz-type proteinase inhibitor homology <BPI>F;212-262/Domain: animal Kunitz-type proteinase inhibitor homology <BPI>F;212-262/Domain: animal Kunitz-type proteinase inhibitor homology <BPI2>
F;29-304/Product: tissue factor pathway inhibitor #status predicted <MAT>
F;54-104/Domain: animal Kunitz-type proteinase inhibitor homology 4BP1>
F;125-175/Domain: animal Kunitz-type proteinase inhibitor homology 4BP2>
F;127-26/Domain: animal Kunitz-type proteinase inhibitor homology 4BP3>
F;54-104,63-87,79-100,125-175,134-158,150-171,217-267,226-250,242-263/Disulfide bonds F;64/Inhibitory site: Lys (coagulation factor VII/tissue factor complex) #status pred F;135/Inhibitory site: Arg (coagulation factor X) #status predicted F;145,195,256/Binding site: carbohydrate (Ann) (covalent) #status predicted F;277/Inhibitory site: Arg (unidentified proteinase) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ó
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Lissue factor pathway inhibitor - rabbit
C.Species: Oryctolagus cuniculus (domestic rabbit)
C.Date: 04-Sep-1997 #sequence_revision 04-Sep-1997 #text_change 13-Aug-1999
C.Accession: 146937 #sequence_revision 04-Sep-1997 #text_change 13-Aug-1999
C.Accession: 146937 #sequence_revision 04-Sep-1997 #text_change 13-Aug-1999
R.Belaaouaj, A.; Kuppuswamy, M.N.; Birktoft, J.J.; Bajaj, S.P.
Thromb. Res. 69, 547-553, 1993
A;Title: Revised cDNA sequence of rabbit tissue factor pathway inhibitor.
A;Reference number: 146937; MuID:93276427; PMID:8503123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                79.8%; Score 91; DB 2; Length 396; 78.3%; Pred. No. 3.6e-05; ive 2; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        67.5%; Score 77; DB 2; Length 299;
76.2%; Pred. No. 0.0024;
tive 1; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 113; DB 1; Length 30
Pred. No. 2.6e-08;
1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A; Status: preliminary; translated from GB/EMBL/DDBJ
```

2 10:49:51 2002

Mon Dec

g

ö

Gaps

ö

```
C;Species: Mycoplasma pulmonis
C;Species: Mycoplasma pulmonis
C;Date: 24-May-2001 #sequence_revision 24-May-2001 #text_change 03-Aug-2001
C;Accession: 690529
K;Chambaud, I:, Heilld, R.; Ferris, S.; Barbe, V.; Samson, D.; Galisson, F.; Moszer, Nucleic Acids Res. 29, 2145-2153, 2001
A;Title: The complete genome sequence of the murine respiratory pathogen Mycoplasma p A;Reference number: A99512; MUID:21267165; PMID:11353084
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       heat shock protein grpe (activation of DNAk) (imported) - Mycoplasma pulmonis (strain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Cross-references: GB:AE001437; PIDN:AAK80430.1; PID:g15025495; GSPDB:GN00168
A;Experimental source: Clostridium acetobutylicum ATCC824
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Cross-references: GB:AL445566; PID:914089556; PIDN:CAC13316.1; GSPDB:GN00153
A;Experimental source: strain UAB CTIP
                                                                                                                                                                                                                                                                                                                                                                                                  A;Residues: 1-4981 <LAW>
A;Cross-references: EMBL:298551; NID:e1331903; PID:e1331910; PIDN:CAB11128.1
                                     Score 52; DB 2; Length 4981;
Pred. No. 91;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 114;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels
                                                                                                                                                                                                                                                                                                                                   A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 49; DB 2;
Pred. No. 7.6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           4217 KKKRRRKKKDSEIKYNSIFNKS 4238
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       4,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 KTKRKKKQRVKIAYEEIFVKN 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     45.6%;
50.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                43.08;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     53.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Local Similarity 50.09
ses 11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              | :||||: :|:||
100 KKSKKRKKETIKVAY 114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 KTKKKKKQRVKIAY 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A; Residues: 1-114 <KUR>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A; Residues: 1-298 <KUR>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Status: preliminary A; Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A; Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A; Accession: C97205
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Map position: 3
A; Note: C0820w
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Gene: CAC2476
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            C; Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     C; Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Genetics
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              qq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ŏ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        q
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ΟŽ
                                                                                                                                                                                                 lipoprotein-associated coagulation inhibitor precursor - rabbit
N'Alternate names: endothelial cell coagulation inhibitor; endothelial cell tissue factor, Species: Orycolagus cuniculus (domestic rabbit)
C'Species: Orycolagus cuniculus (domestic rabbit)
C'Date: 19-Mar-1997 *sequence_revision 19-Mar-1997 *text_change 16-Jul-1999
C'Accession: S12143; A61373
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       R;Colburn, P.; Crabb, J.W.; Buonassist V.
J. Cell. Physiol. 148, 320-326, 1991.
A;Title: Enhanced inhibition of tissue factor by the extended form of an endothelial cel
A;Reference number: A61373; MUID:91349227; PMID:1880157
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A Molecule type: protein
A; Residues: 25-33, 'X', 35-46 <COL>
A; Residues: 25-33, 'X', 35-46 <COL>
C; Superfamily: Lissue factor pathway inhibitor; animal Kunitz-type proteinase inhibitor
C; Keywords: anticoagulant; glycoprotein
E; 50-100/Domain: animal Kunitz-type proteinase inhibitor homology <BPl>
F; 121-171/Domain: animal Kunitz-type proteinase inhibitor homology <BPl>
F; 213-263/Domain: animal Kunitz-type proteinase inhibitor homology <BPS>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Residues: 1-272 <VYS>
A;Cross-references: EMBL:AC003671; NID:92833627; PID:93176675; GSPDB:GN00059; ATSP:F1707
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               hypothetical protein F1707.4 - Arabidopsis thaliana (Species: Arabidopsis thaliana (mouse-ear cress) (Species: Arabidopsis thaliana (mouse-ear cress) (Spacesion: T01999 #sequence_revision 12-Feb-1999 #text_change 04-Mar-2000 (SAccession: T01480 (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ;
0
                                                                                                                                                                                                                                                                                                                                                                               R;Wesselschmidt, R.L.; Girard, T.J.; Broze Jr., G.J.
Nucleic Acids Res. 18, 6440, 1990
A;Title: cDNA sequence of rabbit lipoprotein-associated coagulation inhibitor.
A;Reference number: S12143; MUID:91057146; PMID:2136251
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A; Molecule type: mRNA
A; Residues: 1-300 <WES>
A; Cross-references: EMBL:X54708; NID:g1612; PIDN:CAA38515.1; PID:g1613
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              C; Superfamily: Arabidopsis thaliana hypothetical protein F1707.4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 300;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            49.1%; Score 56; DB 2; Length 272; 40.9%; Pred. No. 1.8;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            67.5%; Score 77; DB 2;
76.2%; Pred. No. 0.0024;
tive 1; Mismatches 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A,Accession: T01480
A,Status: translated from GB/EMBL/DDBJ
A,Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1| :|: | | |:::::|
217 KTDKKKDKMRTKSAHEKLYMRN 238
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      8,
277 KTKRKKKKQPVKITYVETFVK 297
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  278 KTKRKKKKQPVKITYVETFVK 298
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 KTKRKKKQRVKIAYEEIFVKN 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 KTKRKKKQRVKIAYEEIFVK 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Reference number: 214334
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity
9; Conserva
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Gene: ATSP:F1707.4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A; Accession: S12143
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          16;
```

Matches

RESULT 6 T01480

qq ă

ö

Gaps

; 0

A; Gene: MYPU\_1430

RESULT 7

Dp

C; Genetics:

Query Match

g

ö

Gaps

```
C; Species: Homo sapiens (man)
C; Date: 30-Sep-1993 #sequence_revision 21-Jan-1997 #text_change 11-Jan-2000
C; Date: 30-Sep-1993 #sequence_revision 21-Jan-1997 #text_change 11-Jan-2000
C; Accession: JC5020
B; Tsukahara, F; Hattori, M.; Muraki, T.; Sakaki, Y.
J. Biochem. 120, 820-827, 1996
A; Title: Identification and cloning of a novel cDNA belonging to tetratricopeptide re
A; Reference number: JC5020; MUID:97103476; PMID:8947847
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Molecule type: mRNA
A;Residues: 1-2025 <TSU>
A;Residues: 1-2025 <TSU>
A;Cross-references: DDBJ:D84294; NID:g1632761; PIDN:BAA12301.1; PID:d1012977; PID:g16
C;Comment: This protein has three units of a 34-amino-acid repeat which mediate inter
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Gene: CESP:W02B3.2
A;Introns: 88/3; 122/3; 216/2; 352/2; 466/2; 556/1; 600/3; 661/3
C;Superfamily: beta-adrenergic-receptor kinase; pleckstrin repeat homology; protein k
                                                                                                   C;Accession: T48215
R;Bevan, M.; Peters, S.A.; van Staveren, M.; Dirkse, W.; Stiekema, W.; Bancroft, I.; submitted to the Protein Sequence Database, March 2000
A;Reference number: Z24488
A;Accession: T48215
A;Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    hypothetical protein W02B3.2 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 31-Jan-2000
                                   C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 20-Apr-2000 #sequence_revision 20-Apr-2000 #text_change 20-Apr-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DB 2; Length 727;
56;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     42.1%; Score 48; DB 2; Length 231; 45.0%; Pred. No. 20; tive 6; Mismatches 5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Cross-references: EMBL:U22833; PIDN:AAA64322.1; CESP:W02B3.2 A;Experimental source: strain Bristol N2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2; Indels
                                                                                                                                                                                                                                                                                                              A;Molecule type: DNA
A;Residues: 1-231 <BBV>
A;Cross-references: EMBL:AL162351
A;Experimental source: cultivar Columbia; BAC clone T20L15
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       R.Connell, M. submitted to the EMBL Data Library, March 1995
A.Description: The sequence of C. elegans cosmid W02B3.
A.Reference number: 220150
A.Reference number: 220150
A.Recession: T26096
A.Status: preliminary; translated from GB/EMBL/DDBJ
A.Molecule type: DNA
A.Residues: 1-727 < CON>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Map position: 5
A; Introns: 23/3; 57/1; 77/3; 125/2; 173/1; 202/3
A; Note: T20L15.210
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      4; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      42.1%; Score 48;
57.1%; Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    tetratricopeptide repeat protein - human
N; Alternate names: protein T20L15.210
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    3 KRKRKKQRVKIAYEEIFVKN 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       |:|:|||: | ::||:|
32 KKKKKKQKPLIREDDIFFQN 51
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 42.1%
Best Local Similarity 45.0%
Matches 9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 57.1;
Matches 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             541 KKRSKOKIKVAVEE 554
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          4 RKRKKQRVKIAYEE 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Accession: JC5020
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       C; Accession: T26096
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      C; Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    οy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ŏ
                                                                                                                                                                                                                                                                                                                                                                                                                                              conserved hypothetical protein AF1152 - Archaeoglobus fulgidus
C;Species: G6393
C;Accession: G6393
R;Klenk, H.P.; Clayton, R.A.; Tomb, J.F.; White, O.; Nelson, K.E.; Ketchum, K.A.; Dodson.
; Flaischmann, R.D.; Quackenbush, J.; Lee, N.H.; Sutton, G.G.; Gill, S.; Kirkness, E.F.
Glodek, A.; Zhou, L.; Overbeek, R.; Gocayne, J.D.; Weidman, J.F.; McDonald, L.
Nature 390, 364-370, 1997
A;Authors: Utterback, T.; Octton, M.D.; Spriggs, T.; Artiach, P.; Kaine, B.P.; Sykes, S.
Smith, H.O.; Woese, C.R.; Venter, J.C.
A;Title: The complete genome sequence of the hyperthermophilic, sulfate-reducing archaec A;Reference number: A69250; MUID:98049343; PMID:9389475
A;Status: prellminary; nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-357 < KLE>
A;Cross-references: GB:AE001024; GB:AE000782; NID:g2689347; PIDN:AAB90092.1; PID:g264943
C;Superfamily: Methanococcus jannaschii conserved hypothetical protein MJ0041
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   translation initiation factor eIF-2 beta chain-like protein - Arabidopsis thaliana
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           C; Species: Schizosaccharomyces pombe
C; Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 21-Jan-2000
C; Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 21-Jan-2000
C; Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 21-Jan-2000
C; Accession: T38956
A; Reference number: 221820
A; Accession: T38956
A; Status: preliminary: translated from GB/EMBL/DDBJ
A; Molecule type: DNA
A; Molecule type: DNA
A; Molecule type: DNA
A; Residues: 1-138 < CKRD
A; Residues: 1-138 < CKRD
A; Residues: SIPAD: 288056; PIDN: CABI0858.1; GSPDB: GNO0066; SPDB: SPAC5D6.10c
C; Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      very hypothetical protein SPAC5D6.10c - fission yeast (Schizosaccharomyces pombe)
                                                                                                                                              ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ô
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A,Gene: SPDB:SPAC5D6.10c
A,Map position: 1
C,Superfamily: Schizosaccharomyces very hypothetical protein SPAC5D6.10c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ;
0
                                                                                                                                              .;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    42.5%; Score 48.5; DB 2; Length 135; 54.5%; Pred. No. 10; tive 3; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       43.0%; Score 49; DB 2; Length 357; 52.9%; Pred. No. 21; tive 3; Mismatches 5; Indels
                                                                          43.0%; Score 49; DB 2; Length 298; 50.0%; Pred. No. 18; 7; Indels Live 4; Mismatches 7; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      |||:||||:: | | | || || 89 KTKKKRKKEKKK---ETIVEKN 107
                                                                                                                                                                                                                 1 KTKRKKKQRVKIAYEEIFVKN 22
                                                                                                                                                                                                                                                         2 KKIRKKKKEIMKIMKNKILVKN 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 KTKRKKKÇRVKIAYEEIFVKN 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       243 KTERHRKTYRAKVVFEE 259
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 52.97
Best Local 9; Conservative
                                                                                                          Best Local Similarity 50.0
Matches 11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 KTKRKKKQRVKIAYEE 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Best Local Similarity 54.5
Matches 12; Conservative
              A; Genetic code: SGC3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
```

RESULT 11

à g ö

Gaps

RESULT 12 T48215

g ò

```
Appothetical protein STY0378 [imported] - Salmonella enterica subsp. enterica subsp. C. Species: Salmonella enterica subsp. enterica serovar Typhi.

A. Mote: this species has also been called Salmonella typhi.

A. Mote: this species has also been called Salmonella typhi.

C. Date: 09-Nov-2001 #sequence_revision 09-Nov-2001 #text_change 09-Nov-2001

C. Accession: ACO045

R. Parkhill, J.; Dougan, G.; James, K.D.; Thomson, N.R.; Pickard, D.; Wain, J.; Churcher, th. T.; Connerton, P.; Cronin, A.; Davis, P.; Davies, R.M.; Dowd, L.; White, N.; Farrar, S.; Moule, S.; O'Gaorra, P.

A. Authors: Parry, C.; Quail, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; A. Authors: Parry, C.; Quail, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; A. Authors: AB0502; PMID:11677608

A. Accession: ACO545

A. Accession: ACO545

A. Stadues: 1-182 <PAR>
A. Residues: 1-182 <PAR>
A. Residues: 1-182 <PAR>
A. Residues: 1-182 <PAR>
A. Genetics:
A. Genetics:
A. Genetics:
A. Genetics:
A. Genetics:
A. Genetics:
A Map position: 21q22.2
C. Superfamily: unassigned tetratricopeptide repeat proteins; RING finger homology; tetra
F. 231-264/Domain: tetratricopeptide repeat homology <TT1>
F. 265-298/Domain: tetratricopeptide repeat homology <TT2>
F. 299-332/Domain: tetratricopeptide repeat homology <TT3>
F. 1953-2002/Domain: RING finger homology <RNG>
                                                                                                                                                                                                                                                                                                        0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ή;
                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                     0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DB 2; Length 182;
                                                                                                                                                                                                                                 Length 2025;
                                                                                                                                                                                                                              42.1%; Score 48; DB 2; Length 202
50.0%; Pred. No. 1.4e+02;
Live 4; Mismatches 5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 41.7%; Score 47.5; D
Best Local Similarity 36.7%; Pred. No. 19;
Matches 11; Conservative 5; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Search completed: December 2, 2002, 10:04:52 Job time : 5.1194 secs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 KTKR-----KRKKQRVKIAYEEIFVKNM 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  67 KMKRITLQYEIKTKDNGVKILYRDVYMKNL 96
                                                                                                                                                                                                                                                                                                                                                                                            : |:||||: :| |||
1177 RLKKKRKKNIKTKVEEI 1194
                                                                                                                                                                                                                                                                                                                                                              1 KTKRKKKÇRVKIAYEEI 18
                                                                                                                                                                                                                                                            Best Local Similarity 50.0
Matches 9; Conservative
                                                                                                                                                                                                                                     Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                 Op
                                                                                                                                                                                                                                                                                                                                                              δλ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     οy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  q
```

```
GenCore version 5.1.3
Copyright (c) 1993 - 2002 Compugen Ltd.
```

OM protein - protein search, using sw model

December Run on:

2, 2002, 09:59:55; Search time 2.28856 Seconds

(without alignments)
416.837 Million cell updates/sec

US-09-741-106-10

Perfect score:

1 KTKRKKKKQRVKIAYEE1FVKNM 23 Sequence:

Gapop 10.0 , Gapext 0.5 **BLOSUM62** Scoring table:

112892 segs, 41476328 residues Searched:

112892 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Maximum Match 100% Listing first 45 summaries Post-processing: Minimum Match 0% Maximum Match 100%

SwissProt\_40:\* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	scription	P10646 homo sapien	54 macac	Н		Q09639 caenorhabdi	P53804 homo sapien	pachn	Q9x0i6 thermotoga					Q16533 homo sapien				m snm		P81433 buchnera ap		P57335 buchnera ap				Q58524 methanococc	P04775 rattus norv		C	Q9v1t7 pyrococcus		075348 homo sapien	Q9cr51 mus musculu	P14118 homo sapien
SUMMARIES	ID	TFPI_HUMAN	TFPI_MACMU	TFPI_RABIT	YDQA_SCHPO	YR22_CAEEL	TTC3_HUMAN	GYRB_BUCAP	RNC_THEMA			RRPO_LYCVA		SNC1_HUMAN	- 1	KPC1_NEUCR	CAT3_HUMAN	CAT3_MOUSE	Y647_METJA	TRXB_BUCAP	NOP5_HUMAN	FLHA_BUCAI	MFD_HELPY	MFD_HELPJ	YKD5_CAEEL	HELS_METJA	CIN2_RAT	TFPI_RAT	ATRX_DROME	RL23_PYRAB	- 1	VAG1_HUMAN	VAG1_MOUSE	RL19_HUMAN
	DB								П																									
	Query Match Length	304	304	300	135	727	2025	803	240	402	604	2210	667	368	1085	1142	167	167	71	319	529	969	666	1001	1093	1195	2005	302	1311	98	118	118	118	196
dФ	Query	0	99.1	$\sim$	(7	$\alpha$	$^{\circ}$	41.2	40.4	39.5	39.5	39.5	39.0	38.6	37.7	37.7	37.3	37.3	36.8	36.8	36.8	36.8	36.8	36.8	36.8	36.8	36.8		36.4					
	Score	114	113	77	48.5	48	48	47	46	45	45	45	44.5	44		4	'n	42.5									4,	4	41.5				41	41
	Result No.	П	7	m	4	ı, i	ا ف		ω (	ט נ	0 ,	1,	77	13	14 -	15	16	17	18	19	20	$\frac{21}{21}$	22	23	24	52	97	17	28	52	30	31	3.5	33

Q9chu2 lactococcus P10962 saccharomyc	Q9y6k9 h nf-kappab	P54792 homo sapien	Q94x/z ractus norv Q06278 homo sapien	P23116 mus musculu	Q9925U nomo sapien Q8rie4 fusobacteri	P20547 vaccinia vi	O26112 methanobact
MIAA_LACLA MK16 YEAST	NEMO_HUMAN DVL1_HUMAN	DVLL_HUMAN	ADO_HUMAN	IF3A_MOUSE	RS18_FUSNN	YVBG_VACCC	RL23_МЕТТН
				н-		Н	-
294	419	670	1338	1344	72	91	100
36.0	36.0	36.0	36.0	36.0	35.1	35.1	35.1
41	41	41	41	41	40	40	40
34	36	8 6 8 6	40	41	43	44	45

### ALIGNMENTS

```
01-JUL-1989 (Rel. 11, Created)
01-JUL-1989 (Rel. 11, Last sequence update)
15-JUN-2002 (Rel. 11, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Tissue factor pathway inhibitor precursor (TFPI) (Lipoprotein-associated coagulation inhibitor) (LACI) (Extrinsic pathway inhibitor)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         [1]
SEQUENCE FROM N.A. (ISOFORM ALPHA).
MEDLINE-88198127; Pubmed-2452157;
Wun T.-C., Kretzmer K.K., Girard T.J., Miletich J.P., Broze G.J. Jr.;
"Cloning and characterization of a cDNA coding for the lipoprotein-
"Cloning and characterization of a cbwa that it consists of three
associated coagulation inhibitory domains.";
tandem Kunitz-type inhibitory domains.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A. (ISOFORM ALPHA).
MEDLINE-91129227; PubMed=1993173;
Van der Logt C.P.E., Retirama P.H., Bertina R.M.;
"Intron-exon organization of the human gene coding for the lipoprotein-associated coagulation inhibitor: the factor Xa dependent inhibitor of the extrinsic pathway of coagulation.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         "Identification of the 1.4 kb and 4.0 kb messages for the lipoprotein associated coagulation inhibitor and expression of the encoded
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A. (ISOFORM ALPHA).
MEDLINE=91161593; PubMed=2002045;
Girard T.J., Eddy R., Wesselschmidt R.L., Macphail L.A.,
Likert K.M., Byers M.G., Shows T.B., Broze G.J. Jr.;
"Structure of the human lipoprotein-associated coagulation inhibitor gene. Introvexon gene organization and localization of the gene to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Girard T.J., Warren L.A., Novotny W.F., Bejcek B.E., Miletich J.P.,
Broze G.J. Jr.;
"Identification of the 1.4 kb and 4.0 kb messages for the lipoprote."
                                                                                                                                                                                                                                                                                                                                                                                                         Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A. (ISOFORM BETA).
Chang J.-Y., Monroe D.M., Roberts H.R.;
Submitted (AUG-1997) to the EMBL/GenBank/DDBJ databases.
                                                                          304 AA.
                                                                          PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A. (ISOFORM ALPHA).
MEDLINE-89388722; PubMed=2781520;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               J. Biol. Chem. 266:5036-5041(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A. (ISOFORM BETA).
TISSUE=Pancreas;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  hromb. Res. 55:37-50(1989).
                                                                          STANDARD;
                                                                                                                                                                                                                                                                                                                                                                          TFPI OR TFPI1 OR LACI.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NCBI_TaxID=9606;
                                                                          TFPI_HUMAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               chromosome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           protein.
RESULT 1
                                                                                                     ACCOORDING TO THE STATE OF THE
```

Mon Dec

```
This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE-97342711; PubMed-9199408;

Burgering M.J., Orbons L.P., van der Doelen A., Mulders J.,
The second Kunitz domain of human tissue factor pathway inhibitor:
The second Kunitz domain of human tissue factor pathway inhibitor:
Cloning structure determination and interaction with factor Xa.";
J. Mol. Biol. 269:395-407(1997).
I- FUNCTION: INHIBITS FACTOR X (X(A)) DIRECTLY AND, IN A XA-DEPENDENT
WAY, INHIBITS VI(A)/TISSUE FACTOR ACTIVITY, PRESNMABLY BY FORMING
A QUATERNARY X(A)/LACI/VI(A)/TF COMPLEX. IT POSSESSES AN
ANTITHROMBOTIC ACTION AND ALSO THE ABILITY TO ASSOCIATE WITH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LIPOPROTEINS IN PLASMA.

-!- SUBCELLULAR LOCATION: Secreted.
-!- ALTERNATIVE PRODUCTS: 2 isoforms; alpha/TrPIalpha (shown here) and beta/TrPIbeta; are produced by alternative splicing.
-!- TISSUE SPECIFCITY: MOSTLY IN ENDOTHELIAL CELLS.
-!- DOMAIN: THIS INHIBITOR CONTAINS THREE INHIBITORY DOMAINS.
-!- PTM: O-GIYCOSYLATED.
                                                                                                                                                                                                                                                                                                                            CARBOHYDRATE-LINKAGE SITES.
MEDLINE-96224851; Pubmed-8639592;
Nakahara Y., Miyagi M.,
Tsunasawa S., Kato H.;
"Amino acid sequence and carbohydrate structure of a recombinant
human tissue factor pathway inhibitor expressed in Chinese hamster
overy cells: one N-and two O-linked carbohydrate chains are located
between Kunitz domains 2 and 3 and one N-linked carbohydrate chain is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Broze G.J. Jr., Girard T.J., Novotny W.F.; "Regulation of coagulation by a multivalent Kunitz-type inhibitor."; Biochemistry 29:7539-7546(1990).
                                                                                                                                                                              infibirory SITES.

BEDLINE-89181950. PubMed-2927510;

Girard T.J., Marren L.A., Novotny W.F., Likert K.M., Brown S.G.,

Miletich J.P., Broze G.J. Jr.;

Frontchonal significance of the Kunitz-type inhibitory domains of

lipoprotein-associated coagulation inhibitor.";

Nature 338:518-520(1989).
                                                                   MEDLINE-90036996; PubMed-2553722;
Novotny W.F., Girard T.J., Miletich J.P., Broze G.J. Jr.;
"Purification and characterization of the lipoprotein-associated coagulation inhibitor from human plasma.";
J. Biol. Chem. 264:18832-18837(1989).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -1- SIMILARITY: CONTAINS 3 BPTI/KUNITZ INHIBITOR DOMAINS.
Strausberg R.;
Submitted (OCT-2001) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE=91104709; PubMed=2271516;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    JOINED.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        JOINED.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            JOINED.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        JOINED.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             JOINED.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 JOINED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Biochemistry 35:6450-6459(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL; J03225; AAA52022.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STRUCTURE BY NMR OF 121-182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAA59480.1;
AAA59480.1;
AAA59480.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAA59480.1;
AAA59526.1;
AAA59526.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAA59480.1;
AAA59480.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAA59480.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              in Kunitz domain 2
                                                   SEQUENCE OF 29-50.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                M58644;
M58645;
M58646;
M58647;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               M59499;
M59493;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     M58650;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           M58648;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            M58649;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   REVIEW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL;
EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL;
```

```
SISCLC (IN ISOFORM BETA).
MISSING (IN ISOFORM BETA).
V -> M (IN DESNP:5940).
/FTtd=VAR_012004.
K->1: ABOLISHES INHIBITION OF VII(A)/TF.
R->L: ABOLISHES INHIBITION OF X(A).
R->L: ABOLISHES INHIBITION OF X(A).
M->L: ABOLISHES INHIBITION OF X(A).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EFHGPSWCLTPADRGLCRANENRFYYNSVIGKCRPFKYSGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         G -> VTKEGTNDGWKNAAHIYQVFLNAFCIHASMFFLGLD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                Prodom; Pubcocc., SMART; SW0131, KU. 3.
SMART; SW00131, KU. 3.
PROSITE; PS00280; BPTLKUNITZ_1; 3.
PROSITE; PS50279; BPTLKUNITZ_2; 3.
Serine protease inhibitor; Glycoprotein; Repeat; Blood coagulation; Serine protease inhibitor; Glycoprotein; Repeat; Blood coagulation; Signal; Alternative splicing; 3D-structure; Polymorphism.

1 28
                                                                                                                                                                                                                                                                                                              TISSUE FACTOR PATHWAY INHIBITOR.
BPTI/KUNITZ INHIBITOR 1
(VII(A)/TISSUE FACTOR BINDING SITE).
BPTI/KUNITZ INHIBITOR 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
                                                                                                                                                                                                                                                                                                                                                                                                                    REACTIVE BOND (BY SIMILARITY).
BY SIMILARITY.
BY SIMILARITY.
REACTIVE BOND (BY SIMILARITY).
REACTIVE BOND (BY SIMILARITY).
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 304;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 REACTIVE BOND (BY SIMILARITY).
N-LINKED (GLCNAC. .).
O-LINKED.
O-LINKED.
N-LINKED (GLCNAC. .).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
                                                                                                                                                                                                                                                                                                                                                            (FACTOR X(A) BINDING SITE).
BPTI/KONITZ INHIBITOR 3.
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 114; DB 1;
Pred. No. 1.3e-09;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0; Mismatches
           M59495; AAA59526.1; JOINED.
M59496; AAA59526.1; JOINED.
M59497; AAA59526.1; JOINED.
M59498; AAA59526.1; JOINED.
M59498; AAA59526.1; JOINED.
M50498; AAA15514.1; -
                                                                                                                                                                                         Interpro; IPR002223; Kunitz_BPTI.
Pfam; PF00014; Kunitz_BPTI; 3.
PRINTS; PR00759; BASICPTASE.
PRODOM; PD000222; Kunitz_BPTI; 3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            282 KTKRKRKKQRVKIAYEEIFVKNM 304
 AAA59526.1; JOINED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 KTKRKKKQRVKIAYEEIFVKNM 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         35015 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 100.08;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
                                                                                                                                                        GlycoSuiteDB; P10646; -. Genew; HGNC:11760; TFPI.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   64
135
227
                                                                                              PIR; A34315; A34315.
PIR; A60433; A60433.
PIR; S03903; S03903.
                                                                                                                                 PDB; 1ADZ; 25-FEB-98.
PDB; 1TFX; 21-JAN-98.
                                                                                     A28650; TIHUGK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         304 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Best Local Similarity
Matches 23; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      64
135
227
                                                                                                                                                                                                                                                                                                                                                   125
M59494;
                                                                                                                                                                                 MIM; 152310;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ACT_SITE
CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                   DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ACT_SITE
DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    VARSPLIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
                                                                                                                                                                                                                                                                                                                                                                                        DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                      DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                           DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                VARSPLIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               VARIANT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MUTAGEN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MUTAGEN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MUTAGEN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TFPI_MACMU
ID TFPI_MACA
AC Q28864
DT 15-JUL
                                                                                                                                                                                                                                                                                                                                                    DOMAIN
                                                                                                                                                                                                                                                                                                                                                                           DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Matches
                         EMBL;
EMBL;
                                               EMBL;
                                                                       EMBL;
                                                             EMBL;
             EMBL;
                                                                                     PIR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      g
  ŏ
```

ö

304 AA.

PRT;

STANDARD;

TFPI\_MACMU Q28864;

15-JUL-1999 (Rel. 38, Created)

```
This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation. The Buropaen Baloinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                              factor pathway inhibitor (TFPI): comparison with human TFPI.";
J. Biochem. 115:708-714(1994).
-!- FUNCTION: INHIBITS FACTOR (X(A)) DIRECTLY AND, IN A XA-DEPENDENT WAY, INHIBITS VII(A)/TISSUE FACTOR ACTIVITY, PRESUMABLY BY FORMING A QUATERNARY X(A)/LACI/VII(A)/TF COMPLEX. IT POSSESSES AN ANTITHROMBOTIC ACTION AND ALSO THE ABILITY TO ASSOCIATE WITH
15-JUL-1999 (Rel. 38, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Tissue factor pathway inhibitor precursor (TFPI) (Lipoprotein-
associated coagulation inhibitor) (LACI) (Extrinsic pathway inhibitor)
                                                                                                                                                                                                                                              Kamei S., Kamikubo Y., Hamuro T., Fujimoto H., Ishihara M., Yonemura H., Miyamoto S., Funatsu A., Enjyoji K., Abumiya T.; "Amino acid sequence and inhibitory activity of rhesus monkey tissue factor pathway inhibitor (TFPI): comparison with human TFPI.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Serine protease inhibitor; Glycoprotein; Repeat; Blood coagulation;
                                                                                               Macaca mulatta (Rhesus macaque).
Sukaryota; Metazoa; Chordatu; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae;
Cercopithecinae; Macaca
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (VII(A)/TISSUE FACTOR BINDING SITE).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        N-LINKED (GLCNAC. .) (POTEWITAL).
N-LINKED (GLCNAC. .) (POTEWITAL).
N-LINKED (GLCNAC. .) (POTEWITAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (FACTOR X(A) BINDING SITE).
BPTI/KUNITZ INHIBITOR 3.
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
REACTIVE BOND (BY SIMILARITY).
BY SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                                                                              -i- DOMAIN: THIS INHIBITOR CONTAINS THREE INHIBITORY DOMAINS.
-i- PTM: O-GLYCOSYLATED (BY SIMILARITY).
-i- SIMILARITY: CONTAINS 3 BPTI/KUNITZ INHIBITOR DOMAINS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            BY SIMILARITY.
TISSUE FACTOR PATHWAY INHIBITOR.
BPTI/KUNITZ INHIBITOR 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LINKED (GLCNAC. . .) (P. 56E13B3FF16282B0 CRC64:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               BPTI/KUNITZ INHIBITOR 2
                                                                                                                                                                                                                                                                                                                                                                                               LIPOPROTEINS IN PLASMA.
SUBCELLULAR LOCATION: Secreted.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PROSITE; PS00280; BPTI_KUNITZ_1; 3.
PROSITE; PS50279; BPTI_KUNITZ_2; 3.
                                                                                                                                                                                                                                 MEDLINE=94375417; PubMed=8089087;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      interPro; IPR002223; Kunitz_BPTI.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Pfam; PF00014; Kunitz_BPTI; 3.
PRINTS; PR00759; BASICPTASE.
ProDom; PD000222; Kunitz_BPTI; 3.
SMART; SM00131; KU; 3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           35085 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL; S73337; AAB31955.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              28
304
104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            267
104
87
100
100
65
175
117
117
136
267
250
263
                                                                                                                                                                                              SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          304 AA;
                                                                                                                                                                 NCBI_TaxID=9544;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                29
54
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           125
                                                                                 OR TFPI1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            HSSP; P10646;
                                                                                                                                                                                                                   rissue=Liver;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ACT_SITE
DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ACT_SITE
CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ACT_SITE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Signal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CHAIN
```

```
ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Belaaouaj A., Kuppuswamy M.N., Birktoft J.J., Bajaj S.D.,;
"Revised cDNA sequence of rabbit tissue factor pathway inhibitor.";
Thromb. Res. 69:547-553(1993).
-!-FUNCTION: INHIBITS FACTOR X (X/A) DIRECTLY AND, IN A XA-DEPENDENT
WAY, INHIBITS FACTOR X (X/A) DIRECTLY AND, IN A XA-DEPENDENT
WAY, INHIBITS FACTOR X (X/A) DIRECTLY PRESUMABLY BY FORMING
A QUATERNARX X(A)/LAGI/VII(A)/TF COMPLEX. IT POSSESSES AN
ANTITHROMBOTIC ACTION AND ALSO THE ABILITY TO ASSOCIATE WITH
LIPOPROTEINS IN PLASMA.
-!- SUBCELLULAR LOCATION: Secreted.
-!- DOMAIN: THIS INHIBITOR COWTAINS THREE INHIBITORY DOMAINS.
-!- SIMILARITY: CONTAINS 3 BPII/KUNITZ INHIBITOR DOMAINS.
                                                                                                                                                                                                                                                                                                                                                                   TFPI_RABIT STANDARD, PRT, 300 AA.
P19761; 028828;
01-FEB-1991 (Rel. 17, Created)
01-FEB-1992 (Rel. 23, Last sequence update)
16-OGT-2001 (Rel. 40, Last annotation update)
Tissue factor pathway inhibitor precursor (TFPI) (Lipoprotein-associated coagulation inhibitor) (LACI) (Extrinsic pathway inhibitor)
                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Oryctolagus cuniculus (Rabbit).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
                                                                             ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TISSUE-Liver;
MEDLINE-91057146; PubMed-2136251;
Wesselschmidt R.L., Girard T.J., Broze G.J. Jr.;
"CDNA sequence of rabbit lipoprotein-associated coagulation
          Score 113; DB 1; Length 304; Pred. No. 1.8e-09;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Warn-Cramer B.J., Broze G.J. Jr., Komives E.A.; "cDNA sequence of rabbit tissue factor pathway inhibitor.";
                                                                      0; Indels
                                                                         1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Nucleic Acids Res. 20:3548-3548(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Nucleic Acids Res. 18:6440-6440(1990).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRINTS: PR00759; BASICPTASE.
ProDom; PD000222; Kunitz_BPTI; 3.
SMART; SM00131; KU; 3.
PROSITE; PS00280; BPTI_KUNITZ_1; 3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL; X54708; CAA38515.1; ALT_SEQ.
EMBL; SG1902; AAB26836.1; -.
FIF: S12143; S12143.
HSSP; P10646; ITFX.
InterPro; IPR002223; Kunitz_BPTI.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TISSUE=Liver;
MEDLINE=92335027; PubMed=1630940;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TISSUE=Lung;
MEDLINE=93276427; PubMed=8503123;
                                                                                                                                                                        1 KTKRKKKQRVKIAYEEIFVKNM 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               REVISIONS TO 72; 211 AND 218.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Pfam; PF00014; Kunitz_BPTI;
Ouery Match
Best Local Similarity 95.77
Matches 22; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NCBI_TaxID=9986;
                                                                                                                                            δŏ
                                                                                                                                                                                                     g
                                                                                                                                                                                                                                                                                                                                                                                                             A PART A
```

```
ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A Wood V., Gwilliam R., Rajandeam M.A., Lyne M., Lyne R., Stewart A.,

A Brooks W., Gwilliam R., Rajandeam M.A., Lyne M., Lyne R., Stewart A.,

Sgouros J., Peat N., Hayles J., Baker S., Basham D., Bowman S.,

A Brooks W., Connor R., Croin A., Davis P., Feltwell T., Fraser A.,

Collins M., Connor R., Croin A., Harris D., Hidalgo J., Hodgson G.,

Gentles S., Goble A., Hamlin N., Harris D., Hidalgo J., Hodgson G.,

A Holroyd S., Hornsby T., Howarth S., Huckle E.J., Hunt S., Jagels K.,

James K., Jones L., Jones M., Leather S., McDonald S., McLean J.,

A Mooney P., Moule S., Mungall K., Murphy L., Niblett D., Odell C.,

A Mooney P., Moule S., Saunders R., McDonald S., McLearford K., Rutter S., Saunders B.,

Skelton J., Simmonds M., Squares R., Squares S., Stewens K.,

A Taylor K., Taylor R.G., Tivey A., Walsh S.V., Warren T., Whitehead S.,

A Weltjens I., Vanstreels E., Rieger M., Schaefer M., Mueller-Auer S.,

A Gabel C., Fuchs M., Fritze C., Holzer E., Moestl D., Hilbert H.,

B BOIZym K., Langer I., Beck A., Lehrach H., Reinhardt R., Pohl T.M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                         Serine protease inhibitor; Glycoprotein; Repeat; Blood coagulation;
                                                                                                                                        (VII(A)/TISSUE FACTOR BINDING SITE).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        .
0
                                                                                            TISSUE FACTOR PATHWAY INHIBITOR.
                                                                                                                                                                                                                                                                                                                                 REACTIVE BOND (BY SIMILARITY)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 300;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      4; Indels
                                                                                                                                                                                      (FACTOR X(A) BINDING SITE).
BPTI/KUNITZ INHIBITOR 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota, Fungi, Ascomycota, Schizosaccharomycetes, Schizosaccharomycetales; Schizosaccharomycetaceae,
                                                                                                                    BPTI/KUNITZ INHIBITOR 1
                                                                                                                                                                BPTI/KUNITZ INHIBITOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       67.5%; Score 77; DB 1; 76.2%; Pred. No. 0.00033;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         15-JUL-1998 (Rel. 36, Created)
15-JUL-1998 (Rel. 36, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Hypothetical protein C5D6.10c in chromosome I.
                                                                                                                                                                                                                                     SIMILARITY).
                                                                                                                                                                                                                                     (BY SIMILARITY BY SIMILARITY. BY SIMILARITY. BY SIMILARITY. BY SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mismatches
                                                                                                                                                                                                                                                                                                                                                     SIMILARITY
SIMILARITY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 pombe (Fission yeast)
  BPTI_KUNITZ_2; 3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE=21848401; PubMed=11859360;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               278 KTKRKKKKQPVKITYVETFVK 298
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 KTKRKKKKQRVKIAYEEIFVK 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STANDARD;
                                                                                                                                                                                                                                                          100
83
96
1171
1171
1132
224
225
227
232
232
                                                                    24
300
100
                                                                                                                                                                                                               263
                                                                                                                                                                   171
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Schizosaccharomyces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Schizosaccharomyces
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             31
269
300 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Local Similarity
nes 16; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
PROSITE; PS50279;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NCBI_TaxID=4896;
                                                                                                                                                                                                            213
                                                                                                                                                                   121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             YDQA_SCHPO
014202;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SPAC5D6.10C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRAIN=972;
                                                                                                                                                                                                                                                                                                                               ACT_SITE
DISULFID
DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ACT_SITE
CARBOHYD
                                                                                                                                                                                                                                                                                                         DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                      ACT_SITE
                                                                                                                                                                                                                                                                                                                                                                                                                                                 DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
                                                                                                                                                                                                                                                             DISULFID
                                                                                                                                                                                                                                                                                   DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                   DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CONFLICT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CONFLICT
                                                                         SIGNAL
                                                                                                                    DOMAIN
                                                                                                                                                                   DOMAIN
                                                                                                                                                                                                                 DOMAIN
                                                   Signal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            YDQA_SCHPO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     THO ACCORDINATION OF THE BEAR READER TO SERVICE AND SE
```

```
This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                            This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               .;
;
                                                                                                                                                                                                                                                               modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
Eger P., Zimmermann W., Wedler H., Wambutt R., Purnelle B., Goffeau A., Cadieu E., Dreano S., Gloux S., Lelaure V., Mottier S., Galibert F., Aves S.J., Xiang Z., Hunt C., Moore K., Hurst S.M., Lucas M., Rochet M., Gaillardin C., Tallada V.A., Garzon A., Thode G., Daga R.R., Cruzado L., Jimmenz J., Sanchez M., del Rey F., Benito J., Dominguez A., Revuelta J.L., Moreno S., Armstrong J., Forsburg S.L., Chertti L., Lowe T., McComble W.R., Paulsen I., Potashkin J., Shpakovski G.V., Ussery D., Barrell B.G., Nurse P.; "The genome sequence of Schizosaccharomyces pombe.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
Rhabditidae; Peloderinae; Caenorhabditis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Submitted (JUL-1995) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-NoV-1995 (Rel. 32, Created)
01-NoV-1995 (Rel. 32, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Putative G protein-coupled receptor kinase W02B3.2 (EC 2.7.1.-).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 48.5; DB 1; Length 135; Pred. No. 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels
                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE 135 AA; 15864 MW; 2F39A1F4A909476D CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     727 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -!- SIMILARITY: CONTAINS 1 RGS DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                    LYS-RICH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            InterPro; IPR001849; PH.
InterPro; IPR000961; Pkinase_C.
InterPro; IPR000942; Regl_Gprotein.
InterPro; IPR002290; Ser_thr_pkinase.
Pfam; PF00069; pkinase; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WormPep; W02B3.2; CE02074.
InterPro; IPR000719; Euk_pkinase.
InterPro; IPR000239; GPCR_kinase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         89 KTKKKKKKKKKK---ETIVEKN 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 KTKRKKKKQRVKIAYEEIFVKN 22
                                                                                                                                                                                                                                                                                                                                                             EMBL; Z98056; CAB10858.1; -. Hypothetical protein. DOMAIN 85 111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL; U22833; AAA64322.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                       42.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 12; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Caenorhabditis elegans.
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      P25098; 1BAK.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GPRK SUBFAMILY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A. STRAIN=Bristol N2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NCBI_TaxID=6239;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     YR22_CAEEL
009639;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Connell M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         q
         δy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         9
```

```
1018
1172
1563
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1899
                                                                                                                                                                                                        MIM; 602259;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GYRB_BUCAP
P29435;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                REPEAT
REPEAT
REPEAT
ZN_FING
DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      VARSPLIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             VARSPLIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DOMAIN
DOMAIN
DOMAIN
DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GYRB_BUCAP
         SO THE TETTE TETTE TO SERVICE SO THE SOUTH THE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          qq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                          Hypothetical protein; Transferase; Serine/threonine-protein kinase; ATP-binding.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE-96281123; PubMed-8724848;
Ohira M., Octsuyama A., Suzuki E., Ichikawa H., Seki N.,
Nagase T., Nomura N., Ohki M.;
"Identification of a novel human gene containing the
tetratricopeptide repeat domain from the Down syndrome region of
chromosome 21.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  J. BLOChem. 120:820-827(1996).
-!- ALTERNATIVE PRODUCTS: 3 ISOFORMS; TRPDI (SHOWN HERE), TPRDII AND TPRDIII; SEEMS TO BE PRODUCED BY ALTERNATIVE SPLICING.
-!- TISSUE SPECIFICITY: FOUND IN ALL TISSUES EXAMINED.
-!- SIMILARITY: CONTAINS 4 TPR REPRATS.
-!- SIMILARITY: CONTAINS 1 RING-TYPE ZINC FINGER.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TISSUE=Fetal brain;
MEDILES=97103476; PubMed=8947847;
TSUKAhara F., Hattori M., Muraki T., Sakaki Y.;
"Identification and cloning of a novel cDNA belonging to tetratricopepitide repeat gene family from Down syndrome-critical recion 21022.2.":
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TTC3_HUMAN STANDARD; PRT; 2025 AA. P53804; P7847; D1-OCT-1996 (Rel. 34, Created) O1-OCT-1996 (Rel. 34, Last sequence update) 16-OCT-2001 (Rel. 40, Last annotation update) Tetratricopeptide repeat protein 3 (TPR repeat protein D).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 48; DB 1; Length 727;
Pred. No. 14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                         AA0530D8A9DA57D7 CRC64;
                                                                                                                                                                                                                                                                                                                                                                            ATP (BY SIMILARITY). ATP (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                 PROTEIN KINASE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  4; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                         BY SIMILARITY
                                                             SMART; SM00233; PH; 1.
SMART; SM00115; RGS; 1.
SMART; SM00133; S_TK_X; 1.
SMART; SM00220; S_TKC; 1.
PROSITE; PS001107; PROTEIN_KINASE_ATP; 1.
PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
PROSITE; PS00108; PROTEIN_KINASE_DOM; 1.
                                                                                                                                                                                                                                                                                                                                   C-TERMINAL.
                                                                                                                                                                                                                                                                                        N-TERMINAL
Pfam; PF00615; RGS; 1.
PRINTS; PR00717; GPCRKINASE.
ProDom; PD000001; Euk_pkinase; 1.
                                                                                                                                                                                                                                                                                                                                                            RGS.
                                                                                                                                                                                                                                                                                                                                                                                                                                            83361 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       42.1%;
57.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  8; Conservative
                                                                                                                                                                                                                          PROSITE; PS50132; RGS; 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    :|| ||::|:|| ||
541 KKRSKQKIKVAVEE 554
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             4 RKRKKQRVKIAYEE 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DNA Res. 3:9-16(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Homo sapiens (Human).
                                                                                                                                                                                                                                                                                        191 4
456 7
54 1
197 2
220 2
318 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                [2]
SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TTC3 OR TPRD
                                                                                                                                                                                                                                                                                                                                                                            NP_BIND
BINDING
ACT_SITE
SEQUENCE
                                                                                                                                                                                                                                                                                                            DOMAIN
DOMAIN
DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      region
                                                                                                                                                                                                                                                                                        DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TTC3_HUMAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    g
    δ
```

```
ö
modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@lsb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
MEDIATR=98184963; PubMed=9516544;
Clark M.A., Baumann L., Baumann P.;
"Sequence analysis of a 34.7-kb DNA segment from the genome of
Buchhera applidicola (endosymbiont of aphids) containing groEL, dnaA,
the atp operon, gidA, and rho.;
Curr. Microbiol. 36:158-163(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 48; DB 1; Length 2025;
                                                                                                                                                                                                                                                                                                                                                                                                                              ARG/LYS-RICH (BASIC).
MISSING (IN ISOFORM TPRDII).
MISSING (IN ISOFORM TPRDIII).
M; 1B4BCAA3684B6253 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Buchnera aphidicola (subsp. Schizaphis graminum).
Bacteria; Proteobacteria; gamma subdivision; Buchnera.
                                                                                                                                                                                                      SMART; SM00184; RING; 1.
SMART; SM00184; RING; 1.
PROSTE; PS0028; TPR; 3.
PROSTE; PS50089; ZF_RING_1; FALSE_NEG.
PROSTE; PS50089; ZF_RING_2; 1.
REPEAT; TPR repeat; Zinc-finger; Alternative splicing.
REPEAT
                                                                                                                                                                                                                                                                                                                                                                                                 ARG/LYS-RICH (BASIC).
ARG/LYS-RICH (BASIC).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-APR-1993 (Rel. 25, Created)
15-DEC-1998 (Rel. 37, Last sequence update)
10-MAY-2000 (Rel. 39, Last annotation update)
DNA gyrase subunit B (EC 5.99.1.3).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    803 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Pred. No. 41;
4; Mismatches
                                                                                                                                                                                                                                                                                                                                         RING-TYPE.
                                                                                                                                                                                                                                                                                                                                                        POLY-SER.
POLY-LYS.
                                                                                                                                                                                                                                                                                                                                                                                       POLY-LYS
                                                                                                                                                                                                                                                                                              TPR 2.
TPR 3.
TPR 4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ΜM,
                                                                                                                                               InterPro; IPR001440; TPR.
InterPro; IPR001841; Znf_ring.
Pfam; PF00007; zf-C3HC4; 1.
Pfam; PF00515; TPR; 3.
                                                        EMBL; D83077; BAA11769.1; -. EMBL; D84294; BAA12301.1; -. EMBL; D84295; BAA12302.1; -. EMBL; D84296; BAA12303.1; -. Genew; HGNC:12393; TTC3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 : |:||||: :| ||||
1177 RLKKKRKKKNIKTKVEEI 1194
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          229889
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 50.000
Best Local 9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 KTKKKKKQRVKIAYEEI 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE OF 1-91 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STANDARD;
                                                                                                                                                                                                                                                                                                         572
609
1997
                                                                                                                                                                                                                                                                                                                                                        456
1029
1902
1029
1185
                                                                                                                                                                                                                                                                                                                                                                                                                                                             310
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NCBI_TaxID=98794;
                                                                                                                                                                                                                                                                                                                                       1957
453
1020
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2025
```

```
This SWISS-PROT entry is copyright. It is produced through a collaboration between the SWISS Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ;
0
DNA RINGS, INCLUDING CATENANES AND KNOTTED RINGS.

-!- CATALYTIC ACTIVITY: ATP-dependent breakage, passage and rejoining of double-stranded DNA.
-!- SUBUNIT: MADE UP OF TWO CHAINS. THE A CHAIN IS RESPONSIBLE FOR DNA BREAKAGE AND REJOINING; THE B CHAIN CATALYZES ATP HYDROLYSIS. THE ENZYME FORMS AN A2B2 TETRAMER.
-!- SIMILARITY: BELONGS TO THE TYPE II TOPOISOMERASE FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRAIN-WASH JOSH 3109;
STRAIN-WASH JOSH 3109;
STRAIN-WASH JOSH 3109;
MEDLINE-9928/316; Dubded-10360571;
Nalson K.E., Clayton R.A., Gill S.R., Gwinn M.L., Dodson R.J.,
Haft D.H., Hickey E.K., Peterson J.D., Nelson W.C., Ketchum K.A.,
McDonald L., Utterback T.R., Malek J.A., Linher K.D., Carrett M.M.,
Stewart A.M., Cotton M.D., Pratt M.S., Phillips C.A., Richardson D.,
Heidelberg J., Sutton G.G., Fleischmann R.D., Eisen J.A., White O.,
Salzberg S.L., Smith H.O., Venter J.C., Fraser C.M.,
"Evidence for lateral gene transfer between Archaea and Bacteria from
genome sequence of Thermotoga maritima.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            41.2%; Score 47; DB 1; Length 803; 40.9%; Pred. No. 22; tive 5; Mismatches 8; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Bacteria; Thermotogae; Thermotogae (class); Thermotogales;
Thermotogaceae; Thermotoga.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Topoisomerase; Isomerase; ATP-binding.
SEQUENCE 803 AA; 92678 MW; C88758E8AB5FE6D2 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  30-MAY 2000 (Rel. 39, Created)
30-MAY-2000 (Rel. 39, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Ribonuclease III (EC 3.1.26.3) (RNase III).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              240 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TIGRFAMS; TIGR01059; gyrB; 1.
PROSITE; PS00177; TOPOISOMERASE_II; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        | : | ::||| :|| 547 KNDEEMNKYQIKIALKEIVIKN 568
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL; AF008210; AAC38108.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 KTKRKKKKRKQRVKIAYEEIFVKN 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL; M80817; AAA73151.1; -.
PIR; JC1160; JC1160.
HSSP; P06982; 1AJ6.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Best Local Similarity 40.9
Matches 9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Thermotoga maritima.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NCBI_TaxID=2336;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RNC OR TM1102
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RNC_THEMA
Q9X016;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RNC_THEMA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  g
         $2 \times \times
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           à
```

```
This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
FUNCTION: DIGESTS DOUBLE-STRANDED RNA. INVOLVED IN THE PROCESSING
                                                                                                                                 phosphomonoester.
--- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
--- SIMILARITY: CONTAINS 1 DRBM (DOUBLE-STRANDED RNA-BINDING) DOMAIN.
--- SIMILARITY: CONTAINS 1 RNASE III DOWAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDIINE=94254098; PubMed-8196054; Bonnefoy N., Chalvet F., Hamel P., Slonimski P.P., Dujardin G.; "OXA1, a Saccharomyces cerevisiae nuclear gene whose sequence is conserved from prokaryotes to eukaryotes controls cytochrome oxidase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STRAIN=S280C / AB972;
STRAIN=S280C / AB972;
Dietrich F.S., Mulligan J.T., Hennessey K.M., Allen E., Araujo R., Aviles E., Berno A., Brennan T., Carpenter J., Chen E., Cherry J.M., Chung E., Duncan M., Guzman E., Hartzell G., Hunicke-Smith S., Hyman R., Kayser A., Komp C., Lashkari D., Lew H., Lin D., Mosedale D., Nakahara K., Namath A., Norgren R., Oefner P., Oh C., Petel F.X., Roberts D., Schlam S., Shogren T., Smith V., Taylor P., Wei Y., Yelton M., Botstein D., Davis R.W.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-FEB-1995 (Rel. 31, Created)
01-FEB-1995 (Rel. 31, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Cytochrome oxidase biogenesis protein OXA1, mitochondrial precursor.
OXA1 OR PET1402 OR YER154W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   InterPro; lrrvvvv, pram; pram; pram; pram; pram; prom; prom;
                                      OF RIBOSOMAL RNA PRECURSORS AND OF SOME MRNAS (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Saccharomyces cerevisiae (Baker's yeast).
Eukaryota, Fungi, Ascomycota; Saccharomycotina, Saccharomycetes;
Saccharomycetales, Saccharomycetaceae; Saccharomyces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    40.4%; Score 46; DB 1; Length 240; 38.9%; Pred. No. 8.6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         94330E8898D48A0D CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               402 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                8; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       J. Mol. Biol. 239:201-212(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL; AE001769; AAD36178.1; -.
TIGR; TM1102; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE 240 AA; 27530 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         InterPro; IPR001159; DS_RBD.
InterPro; IPR000999; RNase_3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  218 RIKKEAEKEAARIAYEKL 235
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 KTKKKKKÇRVKIAYEEI 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity 38.5.
Rest Local 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NCBI_TaxID=4932;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRAIN-FL100;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     biogenesis.'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               OXA1_YEAST
P39952;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        OXA1_YEAST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 9
    SO THE REPORT OF THE PARTY OF T
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           δ
```

ó

```
pp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           δ
                                                                                                                                                                                                                                                                                                                                                                                                                                  This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ó
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                            Herrmann J.M., Neupert W., Stuart R.A.;

"Insertion into the mitochondrial inner membrane of a polytopic protein, the nuclear-encoded Oxalp.";

EMBO J. 16:2217-2226(1997).

-!- FUNCTION: REQUIRED FOR FOST-TRANSLATIONAL STEP OF CYTOCHROME OXIDASE BIOGENESIS. SEEMS TO INVOLVED IN THE PROTEOLYTIC PROCESSING OF CYTOCHROME OXIDASE SUBURT 2.

-!- SUBCELLULAR LOCATION: Integral membrane protein. Mitochondrial.

-!- SIMILARITY: BELONGS TO THE OXAl / 60 KDA IMP FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MITOCHONDRIAL INTERMEMBRANE (PROBABLE)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MITOCHONDRIAL INTERMEMBRANE (PROBABLE)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MITOCHONDRIAL INTERMEMBRANE (PROBABLE)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Transmembrane; Mitochondrion; Transit peptide.
TRANSIT 42 MITOCHONDRION (POTENTIAL).
CHAIN 43 402 CYTOCHROME OXIDASE BIOGENESIS PROTEIN
                                     SEQUENCE FROM N.A.
MEDLINE=91115677; PubMed=7816036;
Bauer M., Behrens M., Esser K., Michaelis G., Pratje E.;
"PET1402, a nuclear gene required for proteolytic processing of cytochrome oxidase subunit 2 in yeast.";
Mol. Gen. Genet. 245:272-278(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ó
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MITOCHONDRIAL MATRIX (PROBABLE).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MITOCHONDRIAL MATRIX (PROBABLE).
W -> R (IN REF. 1).
108890B8F2EE67ED CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MITOCHONDRIAL MATRIX (PROBABLE)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    39.5%; Score 45; DB 1; Length 402;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              7; Indels
Submitted (DEC-1994) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Y426_HUMAN STANDARD; PRT; 604 AA. 043309; 043324; 16-07-2001 (Rel. 40, Last sequence update) 15-JUN-2002 (Rel. 41, Last annotation update) Hypothetical zinc finger protein KIAA0426.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Pred. No. 21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PROBABLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PROBABLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PROBABLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PROBABLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          InterPro; IPR001708; 60kDa_innermeb.
                                                                                                                                                                                                        MEDLINE=97315163; PubMed=9171337;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ;
9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             44815 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               381 KEKRQNSKIKIVHKSNFINN 400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; X77558; CAA54675.1; -...
EMBL; U1817; AAB64681.1; -...
EMBL; X74456; CAA52465.1; -...
PIR; S47239; S47329.
SGD; S0000956; OXA1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   3 KRKRKKQRVKIAYEEIFVKN 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        35.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Pfam; PF02096; 60KD_IMP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Homo sapiens (Human).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           402 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Best Local Similarity
Matches 7; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      43
131
149
201
219
247
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TRANSMEM
DOMAIN
TRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DOMAIN
TRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DOMAIN
TRANSMEM
                                                                                                                                                                                         TOPOLOGY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             KIAA0426
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CONFLICT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Y426_HUMAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT 10
  REAL TO THE STATE OF THE STATE 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ID DI DI OS OS OS
```

```
This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                            Ishikawa K.-I., Nagase T., Nakajima D., Seki N., Ohira M., Miyajima N., Tanaka A., Kotani H., Nomura N., Ohara O.; "Prediction of the coding sequences of unidentified human genes. VIII. 78 new cDNA clones from brain which code for large proteins in vitro.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                             Submitted (AUG-2001) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: MAY BE INVOLVED IN TRANSCRIPTIONAL REGULATION.
-!- SUBCELLULAR LOCATION: Nuclear (Potential).
-!- SIMILARITY: BELONGS TO THE KRUEPPEL FAMILY OF C2H2-TYPE ZINC-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              .;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SMART; SM00431; LER; I.
SMART; SM00431; LER; I.
PROSTIE; PS0004; SCAN BOX; I.
PROSTIE; PS00028; ZINC_FINGER_C2H2_1; 9.
PROSTIE; PS50157; ZINC_FINGER_C3H2_2; 11.
Hypothetical protein; Transcription regulation; DNA-binding; Zinc_finger; Metal-binding; Nuclear protein; Repeat.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 45; DB 1; Length 604;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       6A7F8ECB515A7A73 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRT; 2210 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              4; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SCAN BOX.
ZINC FINGERS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  C2H2-TYPE
C2H2-TYPE
C2H2-TYPE
C2H2-TYPE
C2H2-TYPE
C2H2-TYPE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               C2H2-TYPE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    C2H2-TYPE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -!- SIMILARITY: CONTAINS 1 SCAN BOX.
                                                                                                                                                    MEDLINE=98116655; PubMed=9455477;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL; AB007886; BAA24856.1; -.
EMBL; 298745; CAB11428.2; -.
EMSP; POT248; ADAR.
InterPro: IPR003309; Treg_SCAN.
InterPro: IPR000822; Znf_C2H2.
Pfam; PF02003; SZAN: 1.
PRINTS; PR00048; ZINCFINGER.
ProDom; EM0048; ZINCFINGER.
ProDom; EM0048; ZINCFINGER.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       70222 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           39.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                50.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          | :|| | :|| :||
560 KAFRQRKKTSYKEILLKN 577
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            5 KRKKQRVKIAYEEIFVKN 22
                                                                                                                                                                                                                                                                                                              DNA Res. 4:307-313(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Best Local Similarity 50.0
Matches 9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FINGER PROTEINS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       604 AA;
                                                                                                 SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
                                                                                                                              TISSUE-Brain;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RRPO_LYCVA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ZN_FING
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DOMAIN
ZN_FING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ZN_FING
ZN_FING
ZN_FING
ZN_FING
ZN_FING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ZN_FING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RRPO_LYCVA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              G
```

```
Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SNC1_HUMAN
ολ
                                                                                                                                                                                                                                                                                                   This SWISS-PROT entry is copyright. It is produced through a collaboration between the SWISS institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-0CT-1994 (Rel. 30, Created)
01-0CT-1994 (Rel. 30, Last sequence update)
15-JUL-1998 (Rel. 36, Last annotation update)
Glycyl-tRNA synthetase (EC 6.1.1.14) (Glycine--tRNA ligase) (GlyRS).
GRS1 OR YBR12IC OR YBR0917.
                                                                                                                                                                                                                                                       Virology 161̄:448-456(1987̄).
-!- CATALYTIC ACTIVITY: N nucleoside triphosphate = N diphosphate +
                                                                    Lymphocytic choriomeningitis virus (strain Armstrong).
Viruses; ssRNA negative-strand viruses; Arenaviridae; Arenavirus.
NCBI_TaxID=11624;
                                                                                                                                     Salvato M.S., Shimomaye E.M., Oldstone M.B.A.; "The primary structure of the lymphocytic choriomeningitis virus gene encodes a putative RNA polymerase."; Virology 169:377-384(1989).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Saccharomyces cerevisiae (Baker's yeast).
Eukaryota; Fungi; Ascomycota; Saccharomycotias;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   5;
                                                                                                                                                                                            SEQUENCE OF 161-387; 424-619 AND 1646-1906 FROM N.A. MEDLINE-88072084; PubMed=3318094; Singh M.K., Fuller-Pace F.V., Buchmeier M.J., Southern P.J.; "Analysis of the genomic L RNA segment from lymphocytic choriomeningitis virus.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           39.5%; Score 45; DB 1; Length 2210; 50.0%; Pred. No. 1.2e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    470C8E623176AFD3 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Saccharomycetales; Saccharomycetaceae; Saccharomyces NCBI_TaxID=4932;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                L -> Y (IN REF. 2).
Q -> R (IN REF. 2).
K -> E (IN REF. 2).
C -> S (IN REF. 2).
R -> L (IN REF. 2).
P14240;
01-JMN-1990 (Rel. 13, Created)
01-JMN-1990 (Rel. 13, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
RNA polymerase (EC 2.7.7.48).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRT; 667 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  5; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                         PIR; A30181; RRXPLC.
RNA-directed RNA polymerase; Transferase.
                                                                                                                                                                                                                                                                                                                                                                                         EMBL, J04331; AAA66591.1; -.
EMBL, M18381; AAA46258.1; ALT_SEQ.
EMBL, M18382; AAA46259.1; -.
EMBL, M18383; AAA46260.1; ALT_SEQ.
                                                                                                                SEQUENCE FROM N.A.
MEDLINE-89204909; PubMed-2705303;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     254529 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      50.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      393 RNRKKSKVFRKVSFEELF 410
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         4 RKRKKQRV--KIAYEEIF 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Best Local Similarity 50.0
Matches 9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           354
361
382
552
1727
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2210 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A. STRAIN=S288C;
                                                                                                                                                                                                                                                                                 [RNA](N).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SYG_YEAST
P38088;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CONFLICT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CONFLICT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CONFLICT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CONFLICT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CONFLICT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT 12
SYG_YEAST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          á
```

```
This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its web yn ono-profit institutions as long as its content is In no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDINE=96104546; PubMed=8524284;
Yoon J.B., Roeder R.G.;
Yoon J.B., Roeder R.G.;
"Cloning of two proximal sequence element-binding transcription factor subunits (gamma and delta) that are required for transcription of small nuclear RNA genes by RNA polymerases II and III and interact with the TATA-binding protein.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            30-MAY-2000 (Rel. 39, Created)
30-MAY-2000 (Rel. 39, Last sequence update)
30-MAY-2000 (Rel. 39, Last sequence update)
snRNA activating protein complex 43 kDa subunit (SNAPC 43 kDa subunit) (PSE-binding factor gamma subunit) (PSE-binding factor gamma subunit) (PSE-binding factor gamma subunit) (RSE-binding factor gamma subunit)
                    Mannhaupt G., Stucka R., Ehnle S., Vetter I., Feldmann H.; "Analysis of a 70 kb region on the right arm of yeast chromosome II."; Yeast 10:1363-1381(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Henry R.W., Sadowski C.L., Kobayashi R., Hernandez N.;
"A TBP-TAF complex required for transcription of human snRNA genes by
RNA polymerase II and III.";
                                                                                                                             -!- CATALYTIC ACTIVITY: ATP + glycine + tRNA(Gly) = AMP + diphosphate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRINTS; PRO1043; TRNASYNTHGLY.
TIGRRAMS; TIGR00389; GlyS_dimeric; 1.
PROSITE; PS50862; AA_TRNA_LIGRSE_LI:
AMBINGSONEL; ARA_TRNA_LIGRSE_LI:
SEQUENCE 667 AS, 75410 MW; DD59506C0C9F18EF CRC64;
                                                                                                                                                                                                                            -!- SIMILARITY: BELONGS TO CLASS-II AMINOACYL-TRNA SYNTHETASE FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalla, Eutheria, Primates, Catarrhini, Hominidae, Homo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ٠.
م
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            39.0%; Score 44.5; DB 1; Length 667;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               42;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               4; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A., AND PARTIAL SEQUENCE. MEDLINE=95231630; PubMed=7715707;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 KTKRKKKQRVKIA-----YEEIFVK 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SGD; SO000325; GRS1.
InterPro; IPR002106; AAtRNA_ligaseII.
InterPro; IPR004154; HGTP_anticodon.
InterPro; IPR002314; TRNA-synt_2b.
InterPro; IPR002315; tRNA-synt_gly.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Pfam; PF00587; tRNA-synt_2b; 1.
Pfam; PF03129; HGTP_anticodon; 1.
MEDLINE=95208357; PubMed=7900426;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL, X78993; CAA55623.1; -.
EMBL, 235990; CAA85078.1; -.
PIR; S44700; S44700.
HSSP; P56206; 1B76.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   36.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Nature 374:653-656(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STANDARD;
                                                                                                                                                                + glycyl-tRNA(Gly).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SNC1_HUMAN
Q16533;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
```

Forsburg S.L.,

```
This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its wise by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A Wood V., Gwilliam R., Rajandram M.A., Lyne M., Lyne R., Stewart A.,

RA Wood V., Gwilliam R., Hayles J., Baker S., Basham D., Bownan S.,

RA Brooks K., Brown D., Brown S., Chillingworth T., Churcher C.M.,

RA Gollins M., Connor R., Cronin A., Davis P., Feltwell T., Fraser A.,

RA Gentles S., Goble A., Hamilin N., Harris D., Hidalgo J., Hodgson G.,

RA Holroyd S., Hornsby T., Howarth S., Huckle E.J., Hunt S., Jagels K.,

RA James K., Jones L., Jones M., Leather S., McDonald S., McLean J.,

RA Monney P., Munde S., Mungall K., Murphy L., Niblett D., Odell C.,

RA Nonney P., Moule S., Mungall K., Murphy L., Niblett D., Odell C.,

RA Skelton J., Simmonds M., Squares R., Squares S., Stevens K.,

RA Taylor K., Taylor R.G., Tivey A., Walsh S.V., Warren T., Whitehead S.,

RA Weltjens I., Vanstreels E., Rieger K., Sharp S.,

RA Weltjens I., Vanstreels E., Rieger M., Schaefer M., Muelbert H.,

RA Gabel C., Fuchs M., Fritzc C., Holzer E., Moestl D., Hilbert H.,

RA Borzym K., Langer I., Beck A., Lehrach H., Reinhardt R., Pohl T.M.,

RA Goffeau A., Cadieu E., Dreano S., Gloux S., Lelaure V., Mottier S.,

RA Galibert F., Aves S.J., Xiang Z., Hunt C., Moore K., Hurst S.M.,

RA Daga R.R., Cruzado L., Jimenez J., Sanchez M., del Rey F., Benito J.,
. Cell. Biol. 16:1-9(1996).
PUNCTION: COMPLEX REQUIRED FOR THE TRANSCRIPTION OF BOTH RNA POLYMERASE II AND III SMALL-NUCLEAR RNA GENES. BINDS TO THE PROXIMAL SEQUENCE ELEMENT (PSE), A NON-TATA-BOX BASAL PROMOTER ELEMENT COMMON TO THESE 2 TYPES OF GENES.
SUBUNIT: COMPOSED OF 5 SUBUNITS: SNAP190; SNAP45; SNAP445
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 44; DB 1; Length 368; Pred. No. 27; 8; Mismatches 5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     POLY-GLU.
324E89CF8B540C32 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-FEB-1996 (Rel. 33, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Hypothetical protein C29E6.10c in chromosome I.
SPAC29E6.10c OR SPAC30.14C.
Schizosaccharomyces pombe (Fission yeast).
Eukaryota; Fungl; Ascomycota; Schizosaccharomycetes; Schizosaccharomycetales; Schizosaccharomycetase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE=21848401; PubMed=11859360;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          8;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-FEB-1996 (Rel. 33, Created)
01-FEB-1996 (Rel. 33, Last sequ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DOMAIN 347 352 P
SEQUENCE 368 AA; 42994 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   304 TRKKEKKERLKPAGRKMSLRN 324
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2 TKRKKKKQRVKIAYEEIFVKN 22
                                                                                                                                                                                                                                                                                                                                      EMBL; Z47542; CAA87590.1; -. EMBL; U44754; AAC50358.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   38.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         38.18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 38.10,
Best Local Similarity 38.10,
Best Local Similarity 38.10,
Best Local Similarity 38.10,
                                                                                                                                                                                                                                                                                                                                                                                                 Genew; HGNC:11134; SNAPC1.
MIM; 600591; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                             Franscription regulation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Schizosaccharomyces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                TRANSFAC, T01680
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NCBI_TaxID=4896;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  YAFA_SCHPO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STRAIN=972;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      009863;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               YAFA_SCHPO
    Mol.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         qq
  δ
```

```
This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
Arpaia G., Macino G.;
"Molecular cloning of a protein kinase C homologue from Neurospora
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -!- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 crassa.";
Submitted (MAR-1997) to the EMBL/GenBank/DDBJ databases.
-!- SIMILARITY: CONTAINS 2 ZINC-DEPENDENT PHORBOL-ESTER AND DAG
Dominguez A., Revuelta J.L., Moreno S., Armstrong J., Forsburg Cerrutti L., Lowe T., McCombie W.R., Paulsen I., Potashkin J., Shpakovski G.V., Ussery D., Barrell B.G., Nurse P.; "The genome sequence of Schizosaccharomyces pombe."; Nature 415:871-880(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             .
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Neurospora crassa.
Eukaryota; Fungi, Ascomycota; Pezizomycotina; Sordariomycetes;
Sordariales; Sordariaceae; Neurospora.
NCBI_TaxID=5141;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 43; DB 1; Length 1085;
Pred. No. 1.2e+02;
6; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                EMBL; Z66525; CAA91432.1; -.

EMBL; AL136538; CAB66473.1; -.

Hypothetical protein.

DOMAIN 184 194 POLY-LYS.

DOMAIN 695 698 POLY-CLU.

DOMAIN 718 717 POLY-GLU.

DOMAIN 718 717 POLY-GLU.

DOMAIN 718 711 POLY-GRG.

DOMAIN 938 941 POLY-SER.

SEQUENCE 1085 AA; 122940 MW; 041164132676F233 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      15-JUL-1999 (Rel. 38, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Protein kinase C-like (EC 2.7.1.-).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRT; 1142 AA.
                                                                                             -! - SIMILARITY: TO YEAST YNL091W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             InterPro; IPR002219; DAG_PE-bind.
InterPro; IPR000719; Euk_pkinase.
InterPro; IPR000961; Pkinase_C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   InterPro; IPR000961; Pkinase_C.
InterPro; IPR000861; REM_repeat.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                15-JUL-1999 (Rel. 38, Created)
15-JUL-1999 (Rel. 38, Last seq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL; Y12002; CAA72731.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       37.78;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         47.18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  594 KEKKRDKKKQLKLAKEE 610
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 KTKKKKKKQRVKIAYEE 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             InterPro; IPR000008; C2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         HSSP; 063450; 1A06
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PKC SUBFAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                KPC1_NEUCR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              KPC1_NEUCR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               δλ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Dp
```

```
ö
Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 37.7%; Score 43; DB 1; Length 1142; Best Local Similarity 31.8%; Pred. No. 1.2e+02; Matches 7; Conservative 7; Mismatches 8; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 KTKRKKKKQRVKIAYEEIFVKN 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ò
                     DRANG WAY WAY WAY A COLOR OF A CO
```

Search completed: December 2, 2002, 10:02:50 Job time : 3.28856 secs

:||: || :|: :| 835 ETKKSRKLYAIKVLKKEFIIEN 856

```
(without alignments)
575.215 Million cell updates/sec
                                                                                                                         December 2, 2002, 10:00:15 ; Search time 8.23881 Seconds
                      Compugen Ltd.
GenCore version 5.1.3
Copyright (c) 1993 - 2002 Compud
                                                                                                                                                                                                                                                                                                                                                                                                      Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                 671580 seqs, 206047115 residues
                                                                                                                                                                                                                                                        1 KTKRKKKKQRVKIAYEEIFVKNM 23
                                                                               OM protein - protein search, using sw model
                                                                                                                                                                                                                                                                                                  BLOSUM62
Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                               US-09-741-106-10
                                                                                                                                                                                                             Title:
Perfect score:
                                                                                                                                                                                                                                                                                                  Scoring table:
                                                                                                                                                                                                                                                                                                                                                                 Searched:
                                                                                                                                                                                                                                                        Sequence:
```

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries sp\_vertebrate:\*
sp\_unclassified:\* sp\_fung1:\*
sp\_human:\*
sp\_invertebrate:\*
sp\_mammal:\* sp\_mhc:\* sp\_organelle:\* sp\_archea:\* sp\_bacteria:\* sp\_plant:\* sp\_rodent:\* sp\_virus:\* sb\_phage:\* SPTREMBL\_21:\* Database:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

sp\_rvirus:\*
sp\_bacteriap:\*

sp\_archeap:\*

SUMMARIES

			Description	OS8874 canis famil	O64594 arabidonsis	077372 plasmodium	099566 homo sanien	Ogbox2 homosanien	099794 homo sarien	OHO	097493 clostridium	O98r67 myconlasma	029113 archaeoglob	Offst8 gnetim gnem	091zv2 arahidonsis	09f982 hacillus st	Ogueka homo sanjen	Ogrfv3 salmonalla	Q8zrh4 salmonella
SUPPRES			ΙD		064594	077372	099566	09BPX2	099794	P78549	097693	098R67	029113	O9FST8	09LZV2	O9F982	O9UEK4	O9RFV3	Q8ZRH4
			DB	. 9	10	ິນ	4	4	4	4	16	16	17	10	10	~	4	7	16
			Length	396	272	4981	303	304	312	312	114	298	357	142	231	414	1941	162	162
	æ	Query	Match Length DB	79.8	49.1	45.6	43.9	43.9	43.9	43.9	43.0	43.0	43.0	42.1	42.1	42.1	42.1	41.7	41.7
			Score	91	26	52	20	20	20	20	49	49	49	48	48	48	48	47.5	47.5
		Result	No.	П	2	e	4	Ŋ	9	7	80	6	10	11	12	13	14	15	16

Q82921 salmonella Q9bbq4 lotus japon Q8tke0 methanosarc Q96101 trypanosoma Q9tar8 trypanosoma Q9tar8 trypanosoma	Q95rc1 drosophila P79994 gallus gall Q9wy48 thermotoga Q27481 caenorhabdi	099nho mus musculu 090041 gallus gall 048345 anabaena sp 08v1t9 anabaena sp	aquifex a thermoana cydia pom	거도도	Q8xi42 clostridium Q93wp2 chlamydomon Q8wug7 homo sapien Q8wxe1 homo sapien Q95tz9 drosophila O97230 plasmodium
Q82921 Q9BBQ4 Q8TKE0 O96101 Q9TZN8	095RC1 P79994 Q9WY48 Q27481	Q99NHO Q90941 Q48345 Q8YLT9	067097 Q8R5P3 Q91EU8 P70632	09CVB3 09LU74 021282 09HA30 096CL3	Q8X142 Q93WP2 Q8WUG7 Q8WXE1 Q95TZ9
16 117 5 5	5 13 16	11 13 16 16	112	4 4 8 8 1	10 4 4 4 5 2 5 2
182 333 388 725 734	749 766 780 1113	1599 1633 402 413	653 287 84 129	330 532 571 671	712 712 764 791 1029 1410
41.2 41.2 41.2 41.2 41.2	41.2 41.2 41.2 41.2	41.2 41.2 40.8 40.8	8 4 4 0 0 8 0 0 0 0 0 0 0 0 0 0 0 0 0 0		, , , , , , , , , , , , , , , , , , ,
47.5 47 47 47 47	47 47 47 47	9	46.5 46 45 74 75	44444 1000000	4 4 4 4 4 U R R R R R R
118 118 220 22	223 254 265	20 20 30 30	33 33 34 54	383786	4 4 4 4 4 4 5 1 1 C

### ALIGNMENTS

```
MEDLINE-95071310; PubWed=7980463; MEDLINE-95071310; PubWed=7980463; Gairard T.J., Gailani D., Broze G.J.Jr., "Complementary DNA sequencing of canine tissue factor pathway inhibitor reveals a unique nanomeric repetitive sequence between the second and third Kunitz domains."; Blochem. J. 303:923-928(1994).

EMBL: S75369; AAB32443.1; "HSPP; P10646; ITER.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
NCBI_TaxID=9615;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 396;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            79.8%; Score 91; DB 6; Length 396
78.3%; Pred. No. 1.8e-05;
Live 2; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                         SWART; SM00131; KU; 3.
PROSITE: PS00280; BPTL_KUNITZ_1; 3.
PROSITE: PS50279; BPTL_KUNITZ_2; 3.
SETING protease inhibitor.
SEQUENCE 396 AA; 43948 MW; 50F65C8337A003D9 CRC64;
                                               028874;
01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
10-MAR-2002 (TrEMBLrel. 20, Last annotation update)
Tissue factor pathway inhibitor.
Canis familiaris (Dog).
                                  PRT;
                                                                                                                                                                                                                                                                                                                                                         InterPro; IPR002223; Kunitz_BPTI.
Pfam; PF00014; Kunitz_BPTI; 3.
PRINTS; PR00759; BASICPTASE.
ProDom; PD000222; Kunitz_BPTI; 3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              374 KTKRKKKQTVKIVYEKIFVKKL 396
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 KTKRKKKÇRVKIAYEEIFVKNM 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              18; Conservative
                                PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
                                028874
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Matches
RESULT 1
Q28874
                                  δ
```

ó

П

ô

```
SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NON_TER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Q9BPX2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Q9BPX2
                                                                                                                                                                                                                                                                                                                  099566
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Best Loca
Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT 5
                                                                                                                                                                                                                                                                                          RESULT 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Q9BPX2
                                                                                                                                                                                                                                                                                                       099566
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            q
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             δλ
δλ
                                                                                                                                                                                                                                                                                                                                                                                                                      RA KOSSEME L. Chenk R., Kim C.J., Meyers M.C., Shinn P.,
RA KOSSEME L., Carninci P., Dale J.M., Gibson H.A.,
RA Banh J., Bowser L., Carninci P., Dale J.M., Gibson H.A.,
RA Banh J., Hayashlzaki Y., Ishida J., Jiang P.X., Jones T.,
RA Kaniya A., Karlin-Neumann G., Kawai J., Lam B., Lee J.M., Lin J.,
RA Liu S.X., Miranda M., Narusaka M., Nguyen M., Onodera C.S., Palm C.J.,
RA Tang C.C., Toriumi M., Yamada K., Yu G., Yu S., Shinozaki K.,
RA Tang C.C., Toriumi M., Yamada K., R.,
RA Davis R.W., Theologis A., Ecker J.R.;
R. Subinted (JUL-2001) to the EMBL/GenBank/DDBJ databases.
REBL; AC003671; AAC18798.1; -.
DR EMBL; AY045589; AAK73947.1; -.
SEQUENCE 272 AA; 31022 MW; F4783DDB67E714E5 CRC64;
                                                                                                                                             Arabidopsis thaliana (Mouse-ear cress).
Bukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
eurosids II; Brassicales; Brassicacee; Arabidopsis.
                                                                                                                                                                                                                              STRAIN-CV. COLUMBIA; Vysotskaia V.S., Schwartz J.R., Toriumi M., Yu G., Kwan A., Oji O., Vysotskaia V.S., Schwartz J.R., Toriumi M., Yu G., Kwan A., Oji O., Liu S., Li J., Araujo R., Au M., Brendel V., Buehler E., Conway A.B., Conway A.R., Dewar K., Feng J., Kim C., Kurtz D., Li Y., Palm C.J., Shinn P., Sun H., Davis R.W., Ecker J.R., Federspiel N.A., Theologis A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     .
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Bowman S., Lawson D., Basham D., Brown D., Chillingworth T.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      49.1%; Score 56; DB 10; Length 272;
40.9%; Pred. No. 1.8;
tive 8; Mismatches 5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Plasmodium falciparum (isolate 3D7).
Eukaryota: Alveolata: Apicomplexa; Haemosporida; Plasmodium
                                                                                                                                                                                                                                                                                                                    "Arabidopsis thaliana chromosome 1 BAC F1707 sequence.";
                                                                                                                                                                                                                                                                                                                                                                                     Theologis A.; Submitted (JUN-1998) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                  Submitted (DEC-1997) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-NOV-1998 (TrEMBLrel. 08, Created)
01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
01-NAR-2002 (TrEMBLrel. 20, Last annotation update)
Hypothetical 593.3 kDa protein.
PFC0820W, MAL3P6.23.
                                                                            01-AuG-1998 (TrEMBLrel. 07, Created)
01-AuG-1998 (TrEMBLrel. 07, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRT; 4981 AA
                                                    272 AA.
                                                    PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STRAIN-3D7;
MEDLINE-99376085; Pubmed=10448855;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              217 KTDKKKDKMRTKSAHEKLYMRN 238
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 KTKRKKKQRVKIAYEEIFVKN 22
                                                                                                      01-DEC-2001 (TrEMBLrel. 19, 181707.4 (AT1G70420/F1707_4).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 40.9%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRELIMINARY;
                                                    PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                       STRAIN-CV. COLUMBIA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
                                                                                                                                                                                                                           SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NCBI_TaxID=36329;
                                                                                                                                                                                                 NCBI_TaxID=3702;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      077372 077372;
                                                 064594
064594;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 3
077372
                          RESULT 2
                                      064594
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ò
```

```
Churcher C.M., Craig A., Davies R.M, Devlin K., Feltwell T., Gentles S., Gwilliam R., Hamlin N., Harris D., Holroyd S., Hornsby T., Horrocks P., Jagels K., Jassal B., Kyes S., McLean J., Moule S., Minghy L., Oliver K., Quail M.A., Rajandream M.-A., Rutter S., Skelton J., Squares S., Sulston J.E., Whitehead S., Woodward J.R., Newbold C., Barrell B.G., "The complete nucleotide sequence of chromosome 3 of Plasmodium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Homo sapiens (Human).
Sukaryota: Metazooa: Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ö
                                                                                                                                                                                                                                                                                                                                                                                                      Score 52; DB 5; Length 4981; Pred. No. 1e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   43.9%; Score 50; DB 4; Length 303; ilarity 64.3%; Pred. No. 15; Conservative 3; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                       EMBL; 298551; CAB11128.i; -.
Hypothetical protein.
SEQUENCE 4981 AA; 593251 MW; 887515A15E085395 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        7; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Luna L., Bjoras M., Rognes T., Hoff E., Seeberg E.;
Submitted (NOV-1996) to the EMBL/GenBank/DDBJ databases.
EMBL; X09687; CAA70865.1; -.
Interpret PRR00436; EndoIII_HNH.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             303 AA; 33468 MW; 5144295C9BFBC64D CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
Nth (E.coli endonuclease III)-like 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-MAY-1997 (TrEMBLrel. 03, Created)
01-MAY-1997 (TrEMBLrel. 03, Last sequence update)
01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
Endonuclease III homologue 1 (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   303 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        4; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PROSITE; PS01155; ENDONUCLEASE_III_2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 4217 KKKRRKKKDSEIKYNSIFNKS 4238
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 KTKRKKKKQRVKIAYEEIFVKN 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  InterPro; IPR003265; Endo_3c.
InterPro; IPR003651; FeS_bind
Pfam; PF00730; HhH-GPD; 1.
                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 45.6%;
Best Local Similarity 50.0%;
Matches 11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SMART; SM00478; ENDO3c; 1. SMART; SM00525; FES; 1.
                                                                                                                                                                                                                              falciparum .";
Nature 400:532-538(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     3 KRKRKKQRVKIAYE 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              48 KRPRKAORLRVAYE 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Local Similarity
nes 9; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NCBI_TaxID=9606;
```

```
(Human).
                                                                                                                                                                                                                    SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
                                                                                                      NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    IISSUE=PLACENTA;
                                                                         Homo sapiens
                                                                                                                                                                                                                                Ricke D.O.;
                                                                                                                                                                             Deaven L.;
  ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ó
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                   RA SEQUENCE FROM N.A.

RA ASPINWALL R., Rothwell D.G., Roldan-Arjona T., Anselmino C.,

RA Aspinwall R., Rothwell D.G., Roldan-Arjona T., Anselmino C.,

RA Hickson I.D., Cheadle J.P., Sampson J.R., Lindahl T., Harris P.C.,

RA Hickson I.D., Cheadle J.P., Sampson J.R., Lindahl T., Harris P.C.,

RT "Cloning and characterization of a functional human homolog of

RT "Cloning and characterization of a functional human homolog of

RT Escherichia coli endonuclease III.";

RD Proc. Natl. Acad. Sci. U.S.A. 94:109-114(1997).

BREL: U79718; AAB41534.1;

BREL: U79718; AAB41534.1;

BREL: U79718; AAB41534.1;

BREL: PRO040365; Endo_3c.

BREL: ROMO478; ENDO365; Endo_3c.

BRART; SM00478; ENDO36; I.

BRART; SM00478; ENDONUCLEASE_III_2; I.

BRART; SROUGSE; FES; I.

SROUENCE 312 AA; 34341 MW; B01821F89DDE8407 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                    Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
                                                                                                                                                                                                                              .
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           .
0
                                                                                                                                                                                                         Score 50; DB 4; Length 304;
Pred. No. 16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 50; DB 4; Length 312;
Pred. No. 16;
                                                                                                                                                                                                                             2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2; Indels
          Strausberg R.; Submitted (FEB-2001) to the EMBL/GenBank/DDBJ databases.
                                                TISSUE=LUNG;
Strausberg R.;
Submitted (NOV-2000) to the EMBL/GenBank/DDBJ databases.
EMBL; BC003014; AAH03014.1; -.
                                                                                                                                                                                     304 AA; 33569 MW; DA97D508BE3D83F0 CRC64;
                                                                                                                                                                                                                                                                                                                                          01-MAY-1997 (TrEMBLrel. 03, Created)
U-MAY-1997 (TrEMBLrel. 03, Last sequence update)
01-MAR-2002 (TEMBLrel. 20, Last annotation update)
Endonuclease III homolog 1, hNFH1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       312 AA.
                                                                                                                                                                                                                                                                                                                         312 AA.
                                                                                                                                                                                                                             3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          3; Mismatches
                                                                                                                                                                 PROSITE; PS01155; ENDONUCLEASE_III_2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRT;
                                                                                                  InterPro; IPR04036; EndoIII_HhH.
InterPro; IPR00326; Endo_3c.
InterPro; IPR003651; FeS_bind.
Pfam; PF00709; HhH-GPD; I.
                                                                                                                                                                                                         43.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      43.9%;
64.3%;
                                                                                                                                            SMART; SM00478; ENDO3c; 1.
SMART; SM00525; FES; 1.
                                                                                                                                                                                                                              9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Local Similarity 64.3
hes 9; Conservative
                                                                                                                                                                                                                                                                                                                         PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRELIMINARY;
                                                                                                                                                                                                                                                 3 KRKKKKQRVKIAYE 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               3 KRKKKKQRVKIAYE 16
                                                                                                                                                                                                                                                                     48 KRPRKAQRLRVAYE 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  56 KRPRKAQRLRVAYE 69
                                                                                                                                                                                                                  Best Local Similarity
                                       SEQUENCE FROM N.A.
                                                                                                                                                                           Endonuclease
TISSUE=LUNG;
                                                                                                                                                                                      SEQUENCE
                                                                                                                                                                                                          Query Match
                                                                                                                                                                                                                                                                                                                                  099794;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      P78549
                                                                                                                                                                                                                                                                                                                       099794
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Best Loca
Matches
                                                                                                                                                                                                                              Matches
                                                                                                                                                                                                                                                                                                   RESULT 6
Q99794
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            P78549
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ΩI
                                                                                                                                                                                                                                                 ŏ
                                                                                                                                                                                                                                                                     qq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               δλ
 RRC
RRL
RRL
RRA
RRA
DR
DR
DR
DR
KW
KW
KW
```

```
MEDILINE-98370989; PubMed-9705289; Ikeda S., Biswas T., Roy R., Izumi T., Boldogh I., Kurosky A., Sarker A.H., Seki S., Mitra S.

Purification and characterization of human NTH1, a homolog of Escherichia coli endonuclease III. Direct identification of Lys-212 as
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Imal K., Sarker A.H., Akiyama K., Ikeda S., Yao M., Tsutsui K., Shohmori T., Seki S.;
"Genomic structure and sequence of a human homologue (NTHLL/NTH1) of Escherichia coli andonuclease III with those of the adjacent parts of TSC2 and SLC9A3R2 genes.";
Submitted (MAY-1998) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.

Ricke D.O., Bruce D., Mundt M., Doggett N., Munk C., Saunders E.,
Robinson D., Jones M., Buckingham J., Chasteen L., Thompson S.,
Goodwin L., Bryant J., Tesmer J., Meincke L., Longmire J., White S.
Ueng S., Tatum O., Campbell C., Fawcett J., Maltble M., Misra M.,
01-MAY-1997 (TrEMBLrel. 03, Created)
U-NAY-1999 (TrEMBLrel. 10, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
HNTH1 (Endonuclease III homolog) (Nth endonuclease III-like 1) (E.
                                                                                                                                                                                                                                                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE OF 9-312 FROM N.A.
MEDLINE=96180675; PubMed=8611553;
Hilbert T.P., Boorstein R.J., Kung H.C., Bolton P.H., Xing D.,
Cunningham R.P., Teebor G.W.;
"Purification of a mammalian homologue of Escherichia coli
endonuclease III: identification of a bovine pyrimidine hydrate-
thymine glycol DNAse/AP lyase by irreversible cross linking to a
thymine glycol-containing oligoxynucleotide.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              'Large Scale Sequence Analysis and Annotation with the Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Comparison Analysis (SCAN) System.";
Submitted (SEP-1998) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           "Sequencing of Human Chromosome 16p13.3.";
Submitted (SEP-1998) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PROSITE; PS01155; ENDONUCLEASE_III_2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 the active nucleophilic residue.";
J. Biol. Chem. 273:21585-21593(1998).
                                                                                                                                                               COII).
OCTS3 OR HNTH OR NTHL1/NTH1 OR NTHL1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Interpro; IPR004036; EndoIII_HhH.
InterPro; IPR003265; Endo_3c.
InterPro; IPR003861; FeS_bind.
FROM PF00730; HhH-GPD; 1.
SMART; SM00478; ENDO3c; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL; AB014460; BAA32695.1; -. EMBL; AF498098; AAM11786.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE OF 9-312 FROM N.A. TISSUE=BONE MARROW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE OF 9-312 FROM N.A.
```

```
Q9FST8
                                                                                                                                                                                                                                                                                                          a
                                                                                                                                                                                                                                                                                                                                                                                                                                                  A PAC DIA CONTRACT OF CONTRACT
         SO W W SO W
                                                                                                                                                                                                                                                               ŏ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Op
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Qγ
                                                                                                                       ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STRAIN=ATCC 824 / DSM 792 / VKM B-1787;
MEDLINE-21559325; PubMed-11466286;
Moelling J., Breton G., Omelchenko M.V., Makarova K.S., Zeng Q.,
Gibson R., Lee H.M., Dubois J., Qiu D., Hitti J., Wolf Y.I.,
Tatusov R.L., Sabathe F., Doucette-Stamm L., Soucaille P., Daly M.J.,
Bennett G.N., Koonin E.V., Smith D.R.;
"Genome sequence and comparative analysis of the solvent-producing
bacterium (Lostridum acetobutylicum.";
D. Bacteriol. 183:4823-438(2001).

EMBL, AE007746; AAK80430.1;
                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STRAIN=UAB CTIP;
MEDLINE=21267165; PubMed=11353084;
Chambaud I., Heilig R., Ferris S., Barbe V., Samson D., Galisson F.,
Moszer I., Dybvig K., Wroblewski H., Viari A., Rocha E.P.C.,
Blanchard A.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "The complete genome sequence of the murine respiratory pathogen
                                                                                                                       ó
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Clostridium acetobutylicum.
Bacteria; Firmicutes; Bacillus/Clostridium group; Clostridia; Clostridiales; Clostridiaceae; Clostridium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Bacteria; Firmicutes; Bacillus/Clostridium group; Mollicutes;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      43.0%; Score 49; DB 16; Length 114; 53.3%; Pred. No. 8.8;
                                                                       43.9%; Score 50; DB 4; Length 312; 64.3%; Pred. No. 16;
                                                                                                                                                                                                                                                                                                                                                01-0CT-2001 (TrEMBLrel. 18, Created)
01-0CT-2001 (TrEMBLrel. 18, Last sequence update)
01-0CT-2001 (TrEMBLrel. 18, Last annotation update)
Uncharacterized protein, homolog of Spirochaeta aurantia (9::152901).
                                                                                                                       2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    3; Indels
                          34389 MW; 379816A1E0B45050 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         114 AA; 13153 MW; A798B5CD369922DD CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-0cT-2001 (TrEMBLrel. 18, Created)
01-0cT-2001 (TrEMBLrel. 18, Last sequence update)
01-0cT-2001 (TrEMBLrel. 18, Last annotation update)
Heat shock protein GRPE (Activation of DNAK).
MYPU_1430.
                                                                                                                                                                                                                                                                                                                               PRT; 114 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            298 AA.
                                                                                                                    3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      4; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mycoplasma pulmonis.";
Nucleic Acids Res. 29:2145-2153(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mycoplasmataceae; Mycoplasma.
NCBI_TaxID=2107;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Best Local Similarity 53.3
Matches 8; Conservative
                                                                                                                    9; Conservative
                                                                                                                                                                                                                                                                                                                               PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          100 KKSKKKKKETIKVAY 114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 KTKRKKKKQRVKIAY 15
                                                                                                                                                                  3 KRKRKKQRVKIAYE 16
                                                                                                                                                                                            || || || ||:::|||
56 KRPRKAQRLRVAYE 69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mycoplasma pulmonis.
Endonuclease.
SEQUENCE 312 AA;
                                                                                        Best Local Similarity
Matches 9; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Complete proteome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NCBI_TaxID=1488;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE
                                                                         Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Q98R67;
                                                                                                                                                                                                                                                                                                                               097693
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          098R67
                                                                                                                                                                                                                                                                                RESULT 8
Q97G93
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 9
Q98R67
                                                                                                                                                                  δ
                                                                                                                                                                                                             g
                                                                                                                                                                                                                                                                                                                                                     ò
```

```
ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE=98049343; PubMed=9389475; Klenk H.-P., Clayton R.A., Tomb J.-F., White O., Nelson K.E., Klenk H.-P., Clayton R.A., Tomb J.-F., White O., Nelson K.E., Retchum K.A., Dodson R.J., Gwinn M., Hickey E.K., Peterson J.D., Richardson D.L., Kerlavage A.R., Graham D.E., Kyrpides N.C., Fleischmann R.D., Quackenbush J., Lee N.H., Sutton G.G., Gill S., Kirkness E.F., Dougherty B.A., McKenney K., Adams M.D., Loftus B., Peterson S., Reich C.I., McNeil L.K., Badger J.H., Glodek A., Ebu L., Overbeek R., Gocayne J.D., Weidman J.F., McDonald L., Utterback T., Sadow P.W., D'Andrea K.P., Bowman C., Fujii C., Garland S.A., Mason T.M., Olsen G.J., Fraser C.M., Smith H.O., Woese C.R.,
                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The complete genome sequence of the hyperthermophilic, sulphate-
                                                                                                                                                                                                                                  ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 49; DB 17; Length 357;
Pred. No. 25;
3; Mismatches 5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
Putative MADS-domain transcription factor GGM14 (Fragment).
                                                                                                                                                                            Length 298
                                                                                                                                                                                                                                  Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       11GK, MILLIA, THUMP_dom.
Pfam: PF02926; THUMP; 1.
TIGREAMS; TIGR01213; Lemp; 1.
Hypothetical protein; Complete proteome.
SEQUENCE 357 AA; 41287 MW; 63F8EE984337FEEI CRC64;
                                                                                                                             298 AA; 34570 MW; 5E0474F726C28A6F CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Archaea; Euryarchaeota; Archaeoglobi; Archaeoglobales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-JAN-1998 (TrEMBLrel. 05, Created)
01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
                                                                                                                                                                            43.0%; Score 49; DB 16; 50.0%; Pred. No. 21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRT; * 357 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            142 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             reducing archaeon Archaeoglobus fulgidus.";
Nature 390.334-370(1997).
EMBL: AE001024; AAB90092.1; -
                                                                                                                                                                                                                               4; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   / DSM 4304 / ATCC 49558;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-MAR-2001 (TrEMBLrel. 16, Created)
01-MAR-2001 (TrEMBLrel. 16, Last seq
01-MAR-2002 (TrEMBLrel. 20, Last anno
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Archaeoglobaceae; Archaeoglobus
                                                                                                                                                                                                                                                                                                               1 KTKRKKKKQRVKIAYEEIFVKN 22
EMBL; AL445563; CAC13316.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       43.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Hypothetical protein AF1152
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Ouery Match
Best Local Similarity 52.2...
Best Local Similarity 54.2...
                          MypuList; MYPU_1430; -.
InterPro; IPR000740; GrpE.
Pfam; PF01025; GrpE; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            243 KTERHRKTYRAKVVFEE 259
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 KTKRKKKQRVKIAYEE 17
                                                                                                                                                                                                                                  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Archaeoglobus fulgidus.
                                                                                                                                                                                                    Best Local Similarity
                                                                                                     Complete proteome. SEQUENCE 298 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NCBI_TaxID=2234;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Venter J.C.;
                                                                                                                                                                                                                                  11;
                                                                                                                                                                               Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Q9FST8
Q9FST8;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              029113;
                                                                                                                                                                                                                                                                                                                                                                                                                                                              029113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GGM14.
                                                                                                                                                                                                                                  Matches
                                                                                                                                                                                                                                                                                                                                                                                                               RESULT 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT 11
```

```
Zinc-finger.
                                                                                                                                                                                                                                           STRAIN=V;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                             NON_TER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NON TER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           09UEK4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Q9UEK4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Q9UEK4
  g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PAC
DDT
DDT
DDT
REA
REA
REA
REA
REA
REA
DD R
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Arabidopsis thaliana (Mouse-ear cress).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
eurosids II; Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                X MEDILINE_2047295; bubMed=11018150; MEDILINE_2047295; bubMed=11018150; MEDILINE_2047295; bubMed=11018150; MEDILINE_2047295; bubMed=11018150; MEDILINE_2047295; bubMed=11018150; Mediline years ago."; I "MADS-Box Gene diversity in seed plants 300 million years ago."; E Mediline Biol. Evol. 17:1425-1434(2000).

R Mol. Biol. Evol. 17:1425-1434(2000).

R InterPro; IPR002100; TF_Mox.

R InterPro; IPR002100; TF_MADSbox.

R FinterPro; IPR00319; SRF-TF; 1.

R SMART; SM00432; MADS; 1.

R PROSTIE; PS50066; MADS_BOX_2; 1.
             Eukaryofa, Viridiplantae, Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Gnetophyta; Gnetopsida; Gnetales; Gnetaceae, Gnetum.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Bevan M., Terryn N., Ardiles W., Buysshaert C., Dasseville R., De Clerck R., De Keyser A., Neyt P., Rouze P., Van Den Daele H., Villarcoel R., Gielen J., Van Montagu M., Bancroft I., Mewes H.W. Rudd S., Lemcke K., Mayer K.F.X.; Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-OCT-2000 (TrEMBLrel. 15, Created)
01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
Translation initiation factor eIF-2 beta chain-like protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  42.1%; Score 48; DB 10; Length 231; 45.0%; Pred. No. 24;
                                                                                                                                                                                                                                                                                                                                                                                                                                      DB 10; Length 142; 15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EU Arabidopsis sequencing project;
Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
EMBL; AL162351; CAB82764 1; -.
InterPro; IPR002735; EIF5_EIF2B.
Pfam; PF01873; EIF5_EIF2B; 1.
ProDom; PD004078; eIF5_EIF2B; 1.
Initiation factor.
                                                                                                                                                                                                                                                                                                                                                                         NON_TER 1 1 1 SEQUENCE 142 AA; 16555 MW; 87045944F89CC5EF CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       231 AA; 26547 MW; 36AEE3C61B1B5B72 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             .,
O
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    231 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                414 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Pred. No. 15;
5; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                      42.1%; Score 48; 47.4%; Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       3 KRKRKKQRVKIAYEEIFVKN 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  |:|:|||:||32 KKKKKKQKPLIREDDIFFQN 51
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      102 TKRRVLNRKIKLLYEEIHV 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2 TKRKKKKQRVKIAYEEIFV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           [2]
SEQUENCE FROM N.A.
                                                             NCBI_TaxID=3382;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NCBI_TaxID=3702;
Gnetum gnemon.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Q9LZV2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              09F982
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Q9LZV2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT 13
Q9F982
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             δλ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    δλ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Dβ
```

```
ô
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EXILT., ADDONALY INTO M., Sasanuma S., Nohata J., Kawashima K., Ahmad I., Hanaoka F., Murakami Y.;
Ahmad I., Hanaoka F., Murakami Y.;
Ahmad I., Hanaoka F., Murakami Y.;
T.Cloning and characterization of novel gene, DCRRI, expressed from Down's syndrome critical region of human chromosome 21q22.2.";
DNA Seq. 7:153-164(1997).
C. -! SIMILARITY: COWTAINS I RING-TYPE ZINC FINGER.
R EMBL; D83327; BAA23666.1;
R InterPro; IPR001440; TPR.
R Pfam; PF00015; TPR; 3.
R Pfam; PF00015; TPR; 3.
R Pfam; SM00184; RING; 1.
R SMART; SM00184; RING; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  .;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ;
0
                                                                                                                                     Bacteria; Firmicutes; Bacillus/Clostridium group; Bacillales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 1941;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 414;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  42.1%; Score 48; DB 4; Length 194
50.0%; Pred. No. 1.7e+02;
Live 4; Mismatches 5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE 1941 AA; 220196 MW; 1B9D07E926909C63 CRC64;
                                                                                                                                                                                                                                                                                         Vasquez C., Pichuantes S., Saavedra C.;
Vasquez C. (CT-1999) to the EMBL/GenBank/DDBJ databases.
EMBL, AF1986-121, AAG208534.1;
HSSP, Q06128, 10DL.
InterPro; IPR000350; chorismate_bind.
PFIGNTS, PR00095; ANTSWTHASEI.
Propon; PD000779; Chorismate_bind; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        414 AA; 48417 MW; 794714B7FD4E1561 CRC64;
01-MAR-2001 (TrEMBLrel. 16, Created)
01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
P-aninobenzoate synthase (Fragment).
Bacillus stearothermophilus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-WAY-2000 (TrEMBLrel. 13, Created)
1-WAY-2000 (TrEMBLrel. 13, Last sequence update)
01-UNA-2002 (TrEMBLrel. 21, Last annotation update)
DCRRI protein (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             42.1%; Score 48; DB 2; 47.4%; Pred. No. 41;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRT; 1941 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 47.4%; Pred. IN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A. MEDLINE=97396022; PubMed=9254009;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             : |:||||: :| ||||
1093 RLKKKRKKKNIKTKVEEI 1110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         4 KRKKKRRTVSYAYRDWFLQ 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       3 KRKRKKQRVKIAYEEIFVK 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 KTKRKKKKQRVKIAYEEI 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Best Local Similarity
Matches 9; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Best_Local Similarity
Matches 9; Conserv
                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                          NCBI_TaxID=1422;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NCBI_TaxID=9606;
```

•

```
December 2, 2002, 09:59:15 ; Search time 7.61194 Seconds (without alignments) 297.593 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                   908470
GenCore version 5.1.3
Copyright (c) 1993 - 2002 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                         Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                     908470 seqs, 133250620 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                    OM protein - protein search, using sw model
                                                                                                                                                                                                                                                              BLOSUM62
Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                    US-09-741-106-12
86
1 AKLNCRLYRKANKSSKL 17
                                                                                                                                                                                                                                                                                                                                                                                               Minimum DB seq length: 0
Maximum DB seq length: 200000000
                                                                                                                                                                                  Title:
Perfect score:
Sequence:
                                                                                                                                                                                                                                                            Scoring table:
                                                                                                                                                                                                                                                                                                                       Searched:
                                                                                                          Run on:
```

Database :	A Genesed 101002:*
	0010115000000
	1: /SIDS2/qcqdata/qeneseq/qenesed
	7: / SIDS// gcguara/genesed/genesed
	3: /SIDS2/gcgdata/geneseg/geneseg

A_Geneseq_101002:*	1: /SIDS2/gcgdata/geneseq/geneseqp-embl/AA1980.DAT:*	2: /SIDS2/gcgdata/geneseq/geneseqp-emb1/AA1981.DAT:*	3: /SIDS2/gcgdata/geneseg/genesegp-embl/AA1982.DAT:*	4: /SIDS2/gcgdata/geneseq/geneseqp-emb1/AA1983.DAT:*	5: /SIDS2/gcgdata/geneseq/geneseqp-emb1/AA1984.DAT:*	6: /SIDS2/gcgdata/geneseg/genesegp-embl/AA1985.DAT:*	7: /SIDS2/gcgdata/geneseg/genesegp-embl/AA1986.DAT:*	8: /SIDS2/gcgdata/geneseq/geneseqp-embl/AA1987.DAT:*	9: /SIDS2/gcgdata/geneseg/genesegp-emb1/AA1988.DAT:*	10: /SIDS2/gcgdata/geneseq/geneseqp-emb1/AA1989.DAT:*	<pre>11: /SIDS2/gcgdata/geneseq/geneseqp-emb1/AA1990.DAT:*</pre>	12: /SIDS2/gcgdata/geneseq/geneseqp-embl/AA1991.DAT:*	13: /SIDS2/gcgdata/geneseq/geneseqp-embl/AA1992.DAT:*	14: /SIDS2/gcgdata/geneseq/geneseqp-emb1/AA1993.DAT:*	15: /SIDS2/gcgdata/geneseq/geneseqp-embl/AA1994.DAT:*	<pre>16: /SIDS2/gcgdata/geneseq/geneseqp-emb1/AA1995.DAT:*</pre>	17: /SIDS2/gcgdata/geneseq/geneseqp-emb1/AA1996.DAT:*	` 	19: /SIDS2/gcgdata/geneseq/geneseqp-emb1/AA1998.DAT:*	20: /SIDS2/gcgdata/geneseg/genesegp-emb1/AA1999.DAT:*	21: /SIDS2/gcgdata/geneseg/genesegp-emb1/AA2000.DAT:*	22: /SIDS2/gcgdata/geneseg/genesegp-emb1/AA2001.DAT:*	23: /SIDS2/gcgdata/geneseq/genesegp-embl/AA2002.DAT:*	

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Description	Glycosaminoglycan Anti-thrombin III Bleeding tendency Heparin-related pe Mature protein seq Sequence of human Antithrombin III m
SUMMARIES	AAW06883 AAR92268 ABB06704 AAM48117 AAW5940 AAP30445 AAR10381 AAR10383 AAR10384 AAR10384
DB	117 12 12 12 12 12
% Query e Match Length DB	1109 1109 1109 1109 1109 1109 1109 1109
% Query Match	100.0 100.0 100.0 100.0 100.0 100.0 100.0
Score	
Result No.	10 10 10

iii ui	Antithrombin III m Antithrombin III m Antithrombin III m	hrombin III antithrombi			Human antithrombin Human antithrombin		Human antithrombin Human antithrombin		Human antithrombin		-	Human antithrombin	anti	anti	Human antithrombin	anti	anti	anti	anti	antit	anti	c
AAR10380 AAR10382 AAR10385	AAR10385 AAR10387 AAR10388	AAR10389 AAR42895	AAR42896 AAR42897	AAR42899	AAR42900 AAR42901	AAR42902	AAR42903 AAR42904	AAR42905	AAR42906 AAR42907	AAR42908	AAR42909	AAR42911	AAR42912	291	AAR42914 AAR42915	291	291	AAR42918	AAR42933		AAR42935	22
175	122	14	14	14:	14	14	14	14	14	14	74	14	14	14	1 t	14	14	14	14	14	14	21
464 464 464	9999	900	4 6 4 4 6 4 6 4 6 4	999	404	ø,	464	9	464 464	9	464	စ	9		404	464	9	ø	464			464
100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0			00		00
9888	9899	86	8 8 9 9	90	86	86	86	86	0 0 0 0	86	8 8 20 9	86	96	9 0	98	98	86	98	98	98	86	86
11 12 13 14	1111	1 I F	202	1010	24.2	25	27	28	30	31	m m m v	3.4	35	30	38	39			42		44	45

## ALIGNMENTS

~

```
Synthetic.
                                                                                                                                                              Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ABB06704;
                                                                                                                                                                                                  Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT 4
                                                                                                                                                                                                                                                                                                                                                                                  RESULT 3
                                                                                                                                                                                                                                                                                                                                                                                                       ABB06704
                                                                                                                                                                                                                                                                                                                                                                                                                                                                q
                                                                                                                                                                                                                                                                                     δy
ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               used in the construction of the chimeric proteins or muteins of the invention. These proteins comprise one of these heparin binding sites in conjunction with a first, second and third Kunitz-type domain derived from TFPI or TFPI-2. The kunitz-type domain sequences are highly basic and may be involved in cell surface localisation by glycosaminoglycan (including heparin) or phospholipid binding. These muteins have one or
                                                                          A glycosaminoglycan binding peptide (AAW06883) derived from antithrombin III is used in novel chimeric proteins of the formula A-R1-B1-B2-C, where A and C are peptides (AAW06875-79, AAW06883-90) able to bind glycosaminoglycans (Gep. heparin) present on cell surfaces. RI is membrane co-factor protein (MCP) or decay accelerating factor (DAF). R 2 is DAF when RI is MCP or MCP when RI is DAF, and B is a peptide that may have complement inhibitor activity. The chimmeric proteins (see also AAW06882) are directed to cell surfaces where they inhibit complement-mediated cell lysis. They are used to treat and prevent disease states in which complement plays a role, e.g. sepsis, adult respiratory distress syndrome, reperfusion injury and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The sequences given in AAR92266-74 are heparin binding sites which were
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Kunitz-type domain; C-terminal tail; tissue factor pathway inhibitor; TFPI-2; cell surface localisation; glycosaminoglycan; heparin; phospholipid; binding; chimeric protein; mutein; substitution; PI-reactive site; sepsis; septic shock; thrombosis; up-regulation; tissue factor; injury; traama; endotoxin; TNF; cancer; IL-1; tumour necrosis factor; interleukin.
                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Chimeric protein comprising Kunitz-type domains from {\tt TFPI-1} and {\tt --2} - used for the treatment of septic shock and thrombosis disorders
                                                                                                                                                                                                                                                                                                                                                                                                                              .;
0
                                                                                                                                                                                                                                                                                                                                                                                    100.0%; Score 86; DB 17; Length 17; 100.0%; Pred. No. 7.6e-08; ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Anti-thrombin III heparin binding domain.
                                          Disclosure; Page 26; 33pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAR92268 standard; peptide; 17 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 9; Page 11; 68pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               95WO-US09464.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     94US-0286521.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 AKLNCRLYRKANKSSKL 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 AKLNCRLYRKANKSSKL 17
                                                                                                                                                                                                                                                                                                                                                                                                           Best Local Similarity 100.
Matches 17; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Creasey AA, Innis MA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 1996-129394/13.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (CHIR ) CHIRON CORP.
      peptide sequences
                                                                                                                                                                                                                                                                                                                                                    17 AA;
                                                                                                                                                                                                                                                                                                          tissue damage.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       05-AUG-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WO9604378-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               25-JUL-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                30-SEP-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      15-FEB-1996,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAR92268;
                                                                                                                                                                                                                                                                                                                                                  Sequence
                                                                                                                                                                                                                                                                                                                                                                                          Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAR92268
```

ŏ g

```
ö
                                                                                                                                                                                                                                                                                                                                                                 ö
More substitutions exclusively in the P1-reactive site of one or more Kunitz-type domains. The chimeric proteins and muteins may be used in a pharmaceutical composition for the treatment of sepsis, septic shock and thrombosis disorders. The proteins may be generally useful in the treatment of diseases caused by the up-regulation of tissue factor bought on by injury, trauma, endotoxin, TNF, cancer, IL-1 or other agents or conditions.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The present invention describes peptides (I) used in the treatment of bleeding tendency, (I) have haemostatic activity and can be used in the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              bleeding tendency. (I) have haemostatic activity and can be used in the inhibition of bleeding tendency. (I) can be used in the treatment of bleeding tendency assused by the administration of heparin during extracorporeal circulation. The present sequence represents a peptide which is used in the exemplification of the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Bleeding tendency treatment related peptide HBP-3 SEQ ID NO:14.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
                                                                                                                                                                                                                                                                                                                                                                    ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      100.0%; Score 86; DB 23; Length 19; 100.0%; Pred. No. 8.5e-08;
                                                                                                                                                                                                                                                                                                             Length 17;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Novel peptides useful for treatment of bleeding tendency
                                                                                                                                                                                                                                                                                                                                                                    Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Bleeding; inhibition; treatment; haemostatic; heparin;
                                                                                                                                                                                                                                                                                                       100.0%; Score 86; DB 17;
100.0%; Pred. No. 7.6e-08;
ive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Example 1; Page 7; 14pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ABB06704 standard; peptide; 19 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /note= "amidated"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      23-JUN-2000; 2000JP-0189707.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                23-JUN-2000; 2000JP-0189707.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    extracorporeal circulation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 AKLNCRLYRKANKSSKL 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2 AKLNCRLYRKANKSSKL 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                 1 AKLNCRLYRKANKSSKL 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 AKLNCRLYRKANKSSKL 17
                                                                                                                                                                                                                                                                                                                                            Best Local Similarity 100.
Matches 17; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 2002-298299/34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Local Similarity
es 17; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (ITOH-) ITO HAM KK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     19 AA;
                                                                                                                                                                                                                                                      17 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         JP2002003397-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        10-JUN-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   09-JAN-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence
```

```
q
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The present invention relates to a peptide (AAM48111), which has high affinity to heparin. Also claimed are (1) a carrier in which a peptide (AAM48115) is combined; (2) a carrier in which a peptide (AAM48115) is combined; (3) a carrier in which a peptide (AAM48118 and AAM48120) is combined; (4) a method for separating and purifying an antithrombotic active fraction in heparin molecule in which a solution containing heparin itself or a treated product of heparin is contacted to the above carrier, and a heparin antithrombotic active fraction prepared by the above method. The antithrombotic fraction in heparin molecule is useful as an antithrombotic agent. The present peptide was used in the method of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Protein expression; monocotyledon plant cell; glycosylated abhal -antitrypsin; AAT; glycosylated antithrombin III; AATI; human serum albumin; HSA; subtilisin BPN'; treatment; emphysema; antithrombotic; blood replacement.
                                                                                                                                                                                                                                                                                                                                                                                               A heparin-highly affinitive peptide-combined carrier and separation and purification of heparin antithrombotic active fraction -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   100.0%; Score 86; DB 23; Length 19; 100.0%; Pred. No. 8.5e-08; Indels 1ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mature protein sequence of antithrombin III (ATIII).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAW59840 standard; Protein; 432 AA.
                  AAM48117 standard; peptide; 19 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 8; Page 6; 10pp; Japanese.
                                                                                                              Heparin-related peptide HBP-3.
                                                                                                                                                                                                                                                                     06-APR-2000; 2000JP-0104338
                                                                                                                                                                                                                                                                                                     06-APR-2000; 2000JP-0104338
                                                                               04-MAR-2002 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      20-NOV-1998 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2 AKLNCRLYRKANKSSKL 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 AKLNCRLYRKANKSSKL 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  17; Conservative
                                                                                                                                             Heparin; antithrombotic
                                                                                                                                                                                                                                                                                                                                                                WPI; 2002-093138/13.
                                                                                                                                                                                                                                                                                                                                    (ITOH-) ITO HAM KK.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 19 AA;
                                                                                                                                                                                                        JP2001288198-A.
                                                                                                                                                                                                                                        16-OCT-2001.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WO9836085-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  20-AUG-1998
                                                                                                                                                                            Synthetic.
                                                 AAM48117;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Matches
AAM48117
```

δ q 

```
ATILITY. The protein is used to exemplify the invention. The specification describes a method for producing mature heterologous protein in monocotyledonous plant cells. The method comprises transforming the cells with a chimeric gene comprising a monocotyledonous plant cells. The method comprises transforming the cells with a chimeric gene comprising a monocotyledon transcription regulator, inducible either during seed maturation or by addingy/removing a small molecule, DNA encoding the heterologous protein, and DNA encoding a signal peptide, with the signal peptide causing secretion of the protein from the cell. Proteins expressed in this mature glycosylation pattern that significantly increases its serum half-life, mature glycosylated antithrombin III (ATIII), mature human serum albumin characteristics, or mature active subtilish BNN'. These proteins are useful therapeutically (e.g. AAT for treating emphysema, ATIII as many, is more included and the protein contains and the contains and the contains and the protein and the same proteins are useful therapeutically (e.g. AAT for treating emphysema, ATIII as many, is more included the protein and th
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The present sequence represents the mature protein of antithrombin III
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence of human antithrombin III (ATIII) from cDNA clones pA62 and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Expressing mature, glycosylated proteins in monocotyledonous plant cells - from chimeric gene including signal peptide sequence, specifically therapeutic agents and industrial enzymes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ó
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 432;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    100.0%; Score 86; DB 19; 100.0%; Pred. No. 2.1e-06;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Thrombosis; therapy; cardiovascular disorders.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Disclosure; Pages 29-30; 53pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAP30445 standard; Protein; 464 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Location/Qualifiers
                                                                                                                                                                                                                                                                                                                 (PHYT-) APPLIED PHYTOLOGICS INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1..32
/label= signal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (BPN' is used in detergents).
                                                                                                                                   97US-0038168.
97US-0038168.
97US-0038169.
98WO-US03068
                                                                                         97US-0038170
                                                                                                                                                                                                                                                                                                                                                                                                      Rodriguez RL, Sutliff TD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                124 AKENCREYRKANKSSKL 140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            25-MAY-1992 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 AKLNCRLYRKANKSSKL 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Local Similarity 100.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 1998-467179/40.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         N-PSDB; AAV41727
13-FEB-1998;
                                                                                                                                   13-FEB-1997;
13-FEB-1997;
                                                                                         13-FEB-1997;
                                                                                                                                                                                                                        13-FEB-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GB2116183-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   21-SEP-1983.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAP30445;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAP30445
```

```
(ALKU ) AKZO NV
                                                                                                                                                                                                                                                                                                                                                             23-JUN-1990;
                                                                                                                                                                                                                                                                                                                                                                           26-JUN-1989;
                                                                                                                                                                                                                                                                                                                                WO9100291-A.
                                                                                                                                                                                                                               10-APR-1991
                                                                                                                                                                                                                                                                                                                                              10-JAN-1991
                                                                                                                                                                                                                                                                                                                                                                                                           Dijkema R,
                                                                                                                                                                                                                 AAR10383;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Seguence
                                                                                                 Sequence
                                                                                                                Query Match
                                                                                                                                                                                                                                                                                          Region
                                                                                                                               Matches
                                                                                                                                                                                         AAR10383
                                                                                                                                                                                    RESULT
                                                                                                                                                                                                   g
δy
                                                                                                                                                                                                                         ;
0
                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                  415..436
/label= P-region
/note= "substitutions occur in this region which is
positions 383-404 in mature ATIII"
                                                                                                                                           incomplete at the 3' end and pA68 comprises 400 bp from the 3' end, 84 bp 3' untranslated region and a poly(A)tail. Plasmids pAT111-E7 and pA7111-34 (claimed) contain a ligation product (pTA2) of pA62 and pA68 (see AAN30203).
                                                                                                                                                                                                                                                                                                                                                       antithrombin 3; P-region variants; heparin-dependent; Factor Ila;
                                                                                                       Human antithrombin III prod. by genetically modified cells - and corresp. cloning vehicles and expression vectors
                                                                                                                                                                                                                         ö
                                                                                                                                                                                                         Length 464;
                                                                                                                                                                                                                         0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New modified antithrombin III variants - with altered heparin-dependent effect to factors IIa and Xa
                                                                                                                                                                                                         Score 86; DB 4; I
Pred. No. 2.3e-06;
                                                                                                                                                                                                                                                                                                                                                             Factor Xa; meizothrombin; blood coagulation.
                                                                                                                                                                                                                         Mismatches
                                                                                                                                                                                                                                                                                                                                                                            Location/Qualifiers
                                                                                                                                                                                                                                                                                          AAR10381 standard; Protein; 464 AA.
                                                                                                                               Disclosure; Fig 2; 14pp; English.
                                                                                                                                                                                                                         ô
                                                                                                                                                                                                         100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 2; Fig 2; 24pp; English.
              82GB-0006262.
83GB-0005786.
83GB-0005786.
85US-0697178.
83GB-0005786
                                                                                                                                                                                                                                                                                                                                                                                                                                                       90WO-EP01026
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      89EP-0201675
                                                                                                                                                                                                                                                                                                                                       Antithrombin III mutant #2.
                                                                                                                                                                                                                                               156 AKLNCRLYRKANKSSKL 172
                                                                                                                                                                                                                                                                                                                         (first entry)
                                                                                                                                                                                                       Query Match 100.
Best Local Similarity 100.
Matches 17; Conservative
                                                                                                                                                                                                                                       1 AKENCRLYRKANKSSKL 17
                                                    (GETH ) GENENTECH INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 1991-036710/05.
                                                                                 WPI; 1983-766797/38
                                                                                                                                                                                           464 AA;
                                                                    Lawn RM;
                                                                                          N-PSDB; AAN30203
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (ALKU ) AKZO NV.
                                                                                                                                                                                                                                                                                                                                                                                                                                                       23-JUN-1990;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      26-JUN-1989;
02-MAR-1983;
              30-JUL-1982;
03-MAR-1982;
                                     01-FEB-1985;
                                                                                                                                                                                                                                                                                                                        10-APR-1991
                            02-MAR-1983;
                                                                                                                                                                                                                                                                                                                                                                                                                         WO9100291-A
                                                                                                                                                                                                                                                                                                                                                                                                                                        10-JAN-1991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Dijkema R,
                                                                   Bock SC,
                                                                                                                                                                                            Sequence
                                                                                                                                                                                                                                                                                                          AAR10381;
                                                                                                                                                                                                                                                                                                                                                                                     Region
                                                                                                                                                                                                                                                                            RESULT 7
Ω
                                                                                                                                                                                                                                                                                                          õ
```

```
Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      derived from the human prothrombin gene. Sequences known to be physiological substrates for Factor Xa were selected and used to replace the wild-type PvuII-StuI fragment of the original ATIII SUN A sequence (see AAQ10323). The substitutions are Ala(391) to Asp, Ser(394) to Ile and Asn(396) to Glu. (Numbers refer to mature AIIII). The substitutions result in a shift in the heparinseppendent inhibition profile of AIIII towards factors IIa and Xa. See also AAR10380-2 and AAR10384-R10390.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    415..436
/label= P-region
/note= "substitutions occur in this region which is
positions 383-404 in mature ATIII"
Mutations introduced into the ATIII reactive centre P-region are derived from the human prothrombin gene. Sequences known to be physiological substrates for Factor Xa were selected and used to replace the wild-type PvuI-StuI fragment of the original ATIII CDNA sequence (see AAQ10323). The substitutions are (given as positions in mature ATIII): Ala(384) to Glu, Val(389) to Leu, Th(386) to Leu, Ala(387) to Glu, Val(388) to Ser, Val(389) to Tyr and Ala(391) to Asp. The substitutions result in a shift in the heparin-dependent inhibition profile of ATIII towards factors IIa and Xa.
See also AAR10380 and AAR10382-R10390.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          antithrombin 3; P-region variants; heparin-dependent; Factor IIa;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mutations introduced into the ATIII reactive centre P-region are
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 464;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New modified antithrombin III variants - with altered heparin-dependent effect to factors IIa and Xa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                100.0%; Score 86; DB 12;
100.0%; Pred. No. 2.3e-06;
Live 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Factor Xa; meizothrombin; blood coagulation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAR10383 standard; Protein; 464 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 2; Fig 2; 24pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           90WO-EP01026
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               89EP-0201675
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Antithrombin III mutant #4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               156 AKLNCRLYRKANKSSKL 172
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 AKLNCRLYRKANKSSKL 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Local Similarity 100.
nes 17; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Visser A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 1991-036710/05.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              464 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                      464 AA;
```

ολ g

```
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAR10380 standard; Protein; 464 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Example; Fig 5; 24pp; English.
                                                                                                                                                                                                                                                                                                               90WO-EP01026
                                                                                                                                                                                                                                                                                                                                        89EP-0201675.
                                                             Antithrombin III P1' mutant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     III mutant #1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            156 AKLNCRLYRKANKSSKL 172
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          10-APR-1991 (first entry)
                                   10-APR-1991 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 AKLNCRLYRKANKSSKL 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Local Similarity 100.
nes 17; Conservative
                                                                                                                                                                                                         Misc-difference 426..426
                                                                                                                                                                                                                                                                                                                                                                                            Dijkema R, Visser A;
                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 1991-036710/05.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  464 AA;
                                                                                                                                                                                                                                                                                                                                                                  (ALKU ) AKZO NV.
                                                                                                                                                                                                                                                                                                               23-JUN-1990;
                                                                                                                                                                                                                                                                                                                                        26-JUN-1989;
                                                                                                                                                                                                                                                           WO9100291-A
                                                                                                                                                                                                                                                                                     10-JAN-1991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence
          AAR10390;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAR10380;
                                                                                                                                            Region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAR10380
ID AAR1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Key
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ρp
δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ;
0
                                   ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                    Gaps
                                                                                                                                                                                                                                                                                              Location/Qualifiers
415..436
/label- P-region
/note="substitutions occur in this region which is positions 383-404 in mature ATII"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mutations introduced into the ATIII reactive centre P-region are derived from the human prothrombin gene. Sequences known to be physiological substrates for Factor Xa were selected and used to replace the Wild-type PvuII-Stul fragment of the original AIIII CDNA sequence (see AAQ10323). The substitutions are (given as positions in mature AIIII) + Ala(391) to Asp and Ser(394) to Ile. The substitutions result in a shift in the heparin-dependent inhibition profile of AIIII towards factors IIa
                                                                                                                                                                                                                                                           antithrombin 3; P-region variants; heparin-dependent; Factor IIa;
Factor Xa; meizothrombin; blood coagulation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ;
0
                                   0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    100.0%; Score 86; DB 12; Length 464; 100.0%; Pred. No. 2.3e-06; ive 0; Mismatches 0; Indels (
          Length 464;
                                   Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New modified antithrombin III variants - with altered heparin-dependent effect to factors IIa and Xa
         100.0%; Score 86; DB 12; 100.0%; Pred. No. 2.3e-06;
                                 Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   See also AAR10380-3 and AAR10385-R10390
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAR10390 standard; Protein; 464 AA.
                                                                                                                                                     AAR10384 standard; Protein; 464 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        100.08; FLY
                                   ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 2; Fig 2; 24pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                 90WO-EP01026
                                                                                                                                                                                                                                                                                                                                                                                                                                                           89EP-0201675
                                                                          156 AKLNCRLYRKANKSSKL 172
                                                                                                                                                                                                                                 Antithrombin III mutant #5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        156 AKLNCRLYRKANKSSKL 172
                                                                                                                                                                                                       (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 AKLNCRLYRKANKSSKL 17
                                                             1 AKLNCRLYRKANKSSKL 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Best Local Similarity 100.
Matches 17; Conservative
                                   Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Dijkema R, Visser A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 1991-036710/05.
          Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             464 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (ALKU ) AKZO NV.
                                                                                                                                                                                                                                                                                                                                                                                                                                 23-JUN-1990;
                                                                                                                                                                                                                                                                                                                                                                                                                                                           26-JUN-1989;
                                                                                                                                                                                                       10-APR-1991
                                                                                                                                                                                                                                                                                                                                                                               WO9100291-A.
                                                                                                                                                                                                                                                                                                                                                                                                       10-JAN-1991
                                   17;
                                                                                                                                                                               AAR10384;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
                                                                                                                                                                                                                                                                                                  Key
Region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT 10
                                   Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAR10390
ID AAR1
                                                                                                                                            AAR10384
                                                                                                                             RESULT
```

ð

```
substituted. The invention covers the substitution of Ile at this position (= Mutant #10, see AR10389). The nature of the substitution was found to be crucial in conferring inhibitory profile to the ATIII polypeptide. Substitutions (other than Ile) that represent a hydrophilic character predict a specificity of heparin-dependent inhibition towards Factor xa. See also AA210323 and AAR10380-9.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
antithrombin 3; P-region variants; heparin-dependent; Factor IIa;
                                                                                             antithrombin 3; P-region variants; heparin-dependent; Factor IIa; Factor Xa; meizothrombin; blood coagulation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ;
                                                                                                                                                                                                                                                                               /label= Phe, Tyr, Leu, Val, Met, Thr, Gly, Ala /note= "Pl' site"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Ser at position 394 of mature ATIII (=426 in this sequence) is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 464;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                New modified antithrombin III variants - with altered heparin-dependent effect to factors IIa and Xa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           100.0%; Score 86; DB 12;
100.0%; Pred. No. 2.3e-06;
                             Factor Xa; meizothrombin; blood coagulation.
```

```
Claim 2; Fig 2; 24pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Region
                                                                                                                                                                                                                                                                                                                                                           RESULT 13
                                                                                                                                                                                                                                                                                                                                                                    AAR10385
    Dp
                                                                                                                                                                                                                                                                                                                                                                               ò
                                                                                                                                                                                                                                                                                                                                                                                                                    ó
                                                                                                                                                                                                                                                                                                                                                                                                                   0; Gaps
                                                                                                                                                                                                                                  Mutations introduced into the ATIII reactive centre P-region are derived from the human prothrombin gene. Sequences known to be physiological substrates for Factor Xa were selected and used to replace the wild-type PoulI-Stul fragment of the original ATIII The substitutions are AAQ10323). (Numbers are for mature ATIII). The substitutions are AIA(384) to Glu, Ser(385) to Leu, TIII). Thr(386) to Leu, AIA(387) to Glu, New 1388) to Ser, Val(389) to Glu, Pro(377) to Glu, Pro(395) to Ser, Val(389) to Asp, Asn(396) to Ala, Thr(401) to Glu, Phe(402) to Ile and Lys(403) to Asp, Val(400) to Ala, Thr(401) to Glu, Phe(402) to Ile and Lys(403) to Asp, The substitutions result in a shift in the heparin-dependent inhibition profile of AIII towards factors IIa and Xa.
         /label= P-region
/note= "substitutions occur in this region which is
positions 383-404 of mature ATIII)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        415..436
/label= P-region
/note= "substitutions occur in this region which is
positions 383-404 in mature ATIII"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  antithrombin 3; P-region variants; heparin-dependent; Factor IIa; Factor Xa; meizothrombin; blood coagulation.
                                                                                                                                                                                                                                                                                                                                                                                           100.0%; Score 86; DB 12; Length 464; 100.0%; Pred. No. 2.3e-06; Live 0; Mismatches 0; Indels (
                                                                                                                                                                                     New modified antithrombin III variants - with altered heparin-dependent effect to factors IIa and Xa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAR10382 standard; Protein; 464 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Location/Qualifiers
                                                                                                                                                                                                                  Claim 2; Fig 2; 24pp; English.
                                                                                      90WO-EP01026.
                                                                                                          89EP-0201675
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 90WO-EP01026
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Antithrombin III mutant #3.
                                                                                                                                                                                                                                                                                                                                                                                                                                               156 AKINCRLYRKANKSSKL 172
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                    1 AKLNCRLYRKANKSSKL 17
                                                                                                                                                                                                                                                                                                                                                        See also AAR10381-R10390.
                                                                                                                                                                                                                                                                                                                                                                                                                17; Conservative
                                                                                                                                                Dijkema R, Visser A;
                                                                                                                                                                   WPI; 1991-036710/05.
                                                                                                                                                                                                                                                                                                                                                                                                      Best_Local Similarity
Matches 17; Conserv
                                                                                                                                                                                                                                                                                                                                                                           464 AA;
                                                                                                                            (ALKU ) AKZO NV.
                                                                                      23-JUN-1990;
                                                                                                          26-JUN-1989;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                23-JUN-1990;
                                                WO9100291-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             10-APR-1991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WO9100291-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              10-JAN-1991.
                                                                    10-JAN-1991
                                                                                                                                                                                                                                                                                                                                                                           Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAR10382;
                                                                                                                                                                                                                                                                                                                                                                                              Query Match
 Region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 12
AAR10382
õ
                                                                                                                                                                                                                                                                                                                                                                                                                                                       g
```

```
Gaps
                                                                                                                                                                                                                                                                                                              Mutations introduced into the ATIII reactive centre P-region are derived from the human prothrombin gene. Sequences known to be physiological substrates for Factor Xa were selected and used to replace the wild-type PvuII-Stul fragment of the original ATIII CDNA sequence (see AAQL0323). The substitutions are (given as positions in mature ATIII): Ala(391) to Asp, sequence (see AAQL035), to val and Asn(396) to Glu. The substitutions result in a shift in the heparin-dependent inhibition perofile of ATIII towards factors IIa and Xa.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      antithrombin 3; P-region variants; heparin-dependent; Factor IIa;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ó
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 464;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels
                                                                                                                                                                                           New modified antithrombin III variants - with altered heparin-dependent effect to factors IIa and Xa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New modified antithrombin III variants - with altered heparin-dependent effect to factors IIa and Xa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   100.0%; Score 86; DB 12;
100.0%; Pred. No. 2.3e-06;
tive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Factor Xa; meizothrombin; blood coagulation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAR10385 standard; Protein; 464 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Location/Qualifiers
                                                                                                                                                                                                                                                                     Claim 2; Fig 2; 24pp; English.
  89EP-0201675.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     89EP-0201675.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        90WO-EP01026.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Antithrombin III mutant #6.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           156 AKLNCRLYRKANKSSKL 172
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    10-APR-1991 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 100.
Best Local Similarity 100.
Matches 17; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 AKLNCRLYRKANKSSKL 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Dijkema R, Visser A;
                                                                                                                                           WPI; 1991-036710/05.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 1991-036710/05.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        464 AA;
                                                  (ALKU ) AKZO NV.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (ALKU ) AKZO NV.
26-JUN-1989;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     23-JUN-1990;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   26-JUN-1989;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WO9100291-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        10-JAN-1991
                                                                                                Dijkema R,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAR10385;
```

```
;
0
                                                                                                                                                                                                                                    Gaps
           Mutations introduced into the ATIII reactive centre P-region are derived from the human prothrombin gene. Sequences known to be physiological substrates for Factor Xa were selected and used to replace the wild-type PoulI-Stul fragment of the original ATIII cDNA sequence (see AAQ10323). The substitutions (given as positions in mature ATIII) are Ser(394) to Ile and Asn(396) to Glu. The substitutions result in a shift in the heparin-dependent in all inhibition profile of ATIII towards factors Ila and Xa. See also AAR10380-4 and AAR10386-R10390.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         415..436/
/labbl= P-region
/note= "substitutions occur in this region which is
positions 383-404 in mature AIIII"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mutations introduced into the ATIII reactive centre P-region are derived from the human prothrombin gene. Sequences known to be physiological substrates for Factor Xa were selected and used to replace the wild-type Puulr-Stul fragment of the original ATIII cDNA sequence (see AAQ10323). The substitutions are Ala(391) to Asp and Asa(396) to Glu. (Numbers refer to mature ATIII). The substitutions result in a shift in the heparin-dependent inhibition brofile of ATIII towards factors IIa and Xa.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             antithrombin 3; P-region variants; heparin-dependent; Factor IIa;
Factor Xa; meizothrombin; blood coagulation.
                                                                                                                                                                                                                                  0
                                                                                                                                                                                                    Length 464;
                                                                                                                                                                                                                                  Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New modified antithrombin III variants - with altered heparin-dependent effect to factors IIa and Xa
                                                                                                                                                                                                                                  .;
0
                                                                                                                                                                                                 100.0%; Score 86; DB 12; 100.0%; Pred. No. 2.3e-06;
                                                                                                                                                                                                                               0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                     AAR10386 standard; Protein; 464 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 2; Fig 2; 24pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 90WO-EP01026
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                89EP-0201675
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Antithrombin III mutant #7.
                                                                                                                                                                                                                                                                              156 AKLNCRLYRKANKSSKL 172
                                                                                                                                                                                                                                                                                                                                                                                                                                   (first entry)
                                                                                                                                                                                                                                                              1 AKLNCRLYRKANKSSKL 17
                                                                                                                                                                                                                                 Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Visser A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 1991-036710/05.
                                                                                                                                                                                                               Best_Local Similarity
Matches 17; Conser
                                                                                                                                                                     464 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       464 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (ALKU ) AKZO NV.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 23-JUN-1990;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              26-JUN-1989;
                                                                                                                                                                                                                                                                                                                                                                                                                                  10-APR-1991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WO9100291-A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   10-JAN-1991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Dijkema R,
                                                                                                                                                                     Sednence
                                                                                                                                                                                                                                                                                                                                                                                                   AAR10386;
                                                                                                                                                                                                  Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Region
                                                                                                                                                                                                                                                                                                                                        RESULT 14
                                                                                                                                                                                                                                                                                                                                                      AAR10386
δ
                                                                                                                                                                                                                                                                                         g
```

DB 12; Length 464;

100.0%; Score 86;

Query Match

```
ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                     // Alabel= P-region // Alabel= P-region // Alabel= P-region // Alabel= "substitutions occur in this region which is positions 383-404 in mature ATIII"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mutations introduced into the ATIII reactive centre P-region are derived from the human prothrombin gene. Sequences known to be physiological substrates for Factor Xa were selected and used to replace the wild-type PVUII-Stul fragment of the original ATIII CDNA sequence (see AAQ10323). The only substitution is Ala(391) to ASP. (Numbers refer to mature ATIII). The substitution results in a shift in the heparin-dependent inhibition profile of ATIII towards factors IIa and Xa.
See also AAR10380-6 and AAR10388-R10390.
                                                                                                                                                                                                                                                      antithrombin 3; P-region variants; heparin-dependent; Factor IIa; Factor Xa; meizothrombin; blood coagulation.
                          ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ;
;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 464;
                          Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       New modified antithrombin III variants - with altered
           Pred. No. 2.3e-06;
Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     100.0%; Score 86; DB 12;
100.0%; Pred. No. 2.3e-06;
Live 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       heparin-dependent effect to factors IIa and Xa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Search completed: December 2, 2002, 10:02:24
Job time : 8.61194 secs
                                                                                                                                                                                                                                                                                                 Location/Qualifiers
                                                                                                                                             AAR10387 standard; Protein; 464 AA.
100.08; ki
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 2; Fig 2; 24pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                     90WO-EP01026.
                                                                                                                                                                                                                                                                                                                                                                                                                                                              89EP-0201675.
                                                               156 AKLNCRLYRKANKSSKL 172
                                                                                                                                                                                                                             Antithrombin III mutant #8.
                                                                                                                                                                                                   (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           156 AKLNCRLYRKANKSSKL 172
                                                   1 AKLNCRLYRKANKSSKL 17
         Best Local Similarity 100.
Matches 17; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 AKLNCRLYRKANKSSKL 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Dijkema R, Visser A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 1991-036710/05.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Best Local Similarity
Matches 17; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            464 AA;
                                                                                                                                                                                                  10-APR-1991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (ALKU ) AKZO
                                                                                                                                                                                                                                                                                                                                                                                                                                                              26-JUN-1989;
                                                                                                                                                                                                                                                                                                                                                                                                                                   23-JUN-1990;
                                                                                                                                                                                                                                                                                                                                                                               WO9100291-A
                                                                                                                                                                                                                                                                                                                                                                                                          10-JAN-1991
                                                                                                                                                                        AAR10387;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
                                                                                                                                                                                                                                                                                                            Region
                                                                                                                    RESULT 15
                                                                                                                                 AAR10387
                                                                                                                                                            δ
                                                                           QQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    qq
```

			·	
			·	
			·	
				· •
				•
		•		

```
GenCore version 5.1.3 Copyright (c) 1993 - 2002 Compugen Ltd.
```

OM protein - protein search, using sw model

December 2, 2002, 10:02:30 ; Search time 2.79104 Seconds Run on:

(without alignments)
179.212 Million cell updates/sec

US-09-741-106-12 86 Title: Perfect score:

1 AKLNCRLYRKANKSSKL 17 Sequence: BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

262574 seqs, 29422922 residues Searched:

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Issued\_Patents\_AA:\* Database

1: /cgg2\_6/ptcdata/1/iaa/5A\_COMB.pep:\*
2: /cgn2\_6/ptcdata/1/iaa/5B\_COMB.pep:\*
3: /cgn2\_6/ptcdata/1/iaa/6A\_COMB.pep:\*
4: /cgn2\_6/ptcdata/1/iaa/6B\_COMB.pep:\*
5: /cgn2\_6/ptcdata/1/iaa/PCTUS\_COMB.pep:\*
6: /cgn2\_6/ptcdata/1/iaa/PCTUS\_COMB.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	Sequence 12, Appl		12.	8, 7	12,	12,	2, 1	9	9	ω	~	ω,	4	4	4	Sequence 10, Appl	, , ;	ģ	Sequence 1, Appli	9	-	Sequence 6, Appli	28,	13,	13,	8,	315
	Ğ	O,	0,	0,	, vi	0,	0,	0,	0,	O,	U,	0,	0,	U,	0,	U,	0,	U	U,	0,1	(J	O)	U)	01	U)	U	G)	U)
SUMMARIES	ID	US-08-437-841-12	US-08-286-521-12	US-08-436-175-12	US-08-435-149-8	US-08-943-682-12	PCT-US95-09464-12	US-08-046-431A-2	US-08-948-997-6	US-09-348-817A-6	US-08-612-986-8	US-08-361-806A-8	PCT-US95-16806A-8	US-08-273-669-4	US-08-954-724-4	US-08-965-947-4	US-09-675-922-10	US-08-273-669-1	US-08-273-669-6	US-08-954-724-1	US-08-954-724-6	US-08-965-947-1	US-08-965-947-6	US-09-675-922-28	US-08-118-270-13	PCT-US93-08528-13	US-09-238-303-8	US-09-134-001C-3194
	DB	 7	7	7	7	4	Ŋ	7	m	4	٦	T	S	٦	~	7	4	-	Н	7	7	7	7	4	-	Ŋ	4	4
	Query Match Length	 17	17	17	17	17	17	464	465	465	41	41	41	20	20	20	14	20	20	20	20	20	20	22	348	348	498	322
оф	Query	 100.0	100.0	100.0	100.0	100.0	100.0				53.5		53.5	50.0	20.0		47.7	47.7	47.7	47.7	47.7	47.7	47.7	47.7	47.7	47.7	47.7	46.5
	Score	98	98	98	86	98	98	86	80	80	46	46	46	43	43	43	41	41	41	41	41	41	41	41	41	41	41	40
	Result No.	 <b>-</b> 1	2	e	4	S	9	7	80	6	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	56	27

;	;	!				
28	33	45.3	20	_	US-08-273-669-5	Sequence 5, Appli
29	9 8	45.3	20	7	US-08-954-724-5	Ŋ,
30	36	45.3	20	7	US-08-965-947-5	S
31	39	45.3	944	~	US-08-867-941-23	23
32	39	45.3	944	7	US-08-867-941-24	24
33	36	45.3	944	4	US-09-074-658-23	23,
34	39	45.3	944	4	-658-2	24
35	38	44.2	375	4	US-09-252-149B-33	
36	38	44.2	681		US-08-760-615-4	4, 4
37	38	44.2	681		US-08-760-615-6	9
38	37	43.0	20		US-08-273-669-2	
39	37	43.0	20		US-08-273-669-3	'n
40	37	43.0	20	7	US-08-954-724-2	2
41	37	43.0	20	~	-724-	'n
42	37	43.0	20	7	-947-	~
43	37	43.0	20	7	US-08-965-947-3	'n
44	37	43.0	172	4	US-09-071-035-442	442
45	37	43.0	360	4	US-09-286-691-25	25,
					ALIGNMENTS	
RESULT 1						
US-08-437-841-12	841-12	2				
; Sequence 12, Application US/08437841	12, 1	Applicat	ion US	708	437841	
; Patent No	o. 556	53123				
; GENERAL	INFOR	GENERAL INFORMATION:				
; APPLICANT:	CANT:	Innis,		e]		
; APPLICANT:	CANT:	Creasey,		B		
; TITLE OF		INVENTION:		mer	Chimeric Proteins	

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30B
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/437,841 FILING DAIL.
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/286,521
FILING DATE: 05-AUG-1994
ATTORNEY/AGENT INFORMATION:
NAME: Savereide, Paul B.
REGISTRATION NUMBER: 36,914
REPERDNEL/COKET NUMBER: 0990.001
TELECOMMUNICATION INFORMATION:
TELEPHONE: 510-601-2585
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
LENGTH: 17 amino acids
""""" APPLICATION ATTOR

LENGTH: 17 amino acids
"""" APPLICATION ATTOR

LENGTH: 17 amino acids
"""" APPLICATION ATTOR

LENGTH: 17 amino acids NUMBER OF SEQUENCES: 37
CORRESPONDENCE ADDRESS:
ADDRESSE: Chiron Corporation
STREET: 4560 Horton St.
CITY: Emeryville ZIP: 94608
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy of STRANDEDNESS: single MOLECULE TYPE: peptide linear USA CA TOPOLOGY: US-08-437-841-12 COUNTRY:

Gaps ·, Query Match 100.0%; Score 86; DB 1; Length 17; Best Local Similarity 100.0%; Pred. No. 1.4e-07; Matches 17; Conservative 0; Mismatches 0; Indels

ö

1 AKLNCRLYRKANKSSKL 17 = = = = = = = =

ά

1 AKLNCRLYRKANKSSKL 17

```
CLASALLALLALON

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/286,521

FILING DATE: 05-AUG-1994

ATTORNEY/AGENT INFORMATION:

NAME: Savereide, Paul B.

REGISTRATION NUMBER: 36,914

REFERNICE/DOCKET NUMBER: 0990.001

TELEPHONE: 510-601-2585

TELEPHONE: 510-601-2585

INFORMATION FOR SEQ. ID NO: 12: SEQUENCE CHARACTERISTICS:

SEQUENCE CHARACTERISTICS:

LENGTH: 17 amino acids
UMBER: US/08/436,175
09-MAY-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0989.001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-08-435-149-8
; Sequence 8, Application US/08435149
; Patent No. 5866402
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ATTORNEY/AGENT INFORMATION:
NAME: SAVEREIDE, PAUL B.
REGISTRATION NUMBER: 36,914
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     REFERENCE/DOCKET NUMBER: 09
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELEPHONE: (510) 601-2585
TELEFAX: (510) 655-3542
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LENGTH: 17 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 AKLNCRLYRKANKSSKL 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 AKENCREYRKANKSSKE 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELEX: N/A
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 100.
Best Local Similarity 100.
Matches 17; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CITY: EMERYVILLE
STATE: CALIFORNIA
COUMTRY: U.S.A.
ZIP: 94662-8097
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy di
                                                                                                                                                                                                                                                                                                                                                              TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-436-175-12
                                                                                                                                                                                                                                                                                                                                            STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: amino acid
                                                                                                                                                                                                                                                                                                                          TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GENERAL INFORMATION:
                                FILING DATE: 09
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Op
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                100.0%; Score 86; DB 1; Length 17; 100.0%; Pred. No. 1.4e-07; tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: ISPEC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30B
CURRENT APPLICATION DATA: US/08/286,521
FILING DATE: 05-AUG-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-08-436-175-12

Sequence 12, Application US/08436175

Patent No. 5696088

GENERAL INFORMATION:
APPLICANT: Innis, Michael
APPLICANT: Creasey, Abla
TITLE OF INVENTION:
CORRESPONDENCES: 37

CORRESPONDENCE ADDRESS:
ADDRESSEE: Chiron Corporation
STREET: 4560 Horton St.
                                                                  Sequence 12, Application US/08286521
Patent No. 5589359
GENERAL INFORMATION:
APPLICANT: Innis, Michael
APPLICANT: Creasey, Abla
TITLE OF INVENTION: Chimeric Proteins
NUMBER OF SEQUENCES: 37
CORRESPONDENCE ADDRESS:
ADDRESSEE: Chiron Corporation
STREET: 4560 Horton St.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ZIP: 946UB
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: SAVEREIG, Paul B.
REGISTRATION NUMBER: 36,914
REFERENCE/DOCKET NUMBER: 0990
TELECOMMUNICATION INFORMATION:
TELEPHONE: 510-601-2585
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEFAX: 510-655-3542
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   17 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 AKLNCRLYRKANKSSKL 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 AKENCREYRKANKSSKE 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; MOLECULE TYPE: peptide US-08-286-521-12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Best Local Similarity
Matches 17; Conserva
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COUNTRY: US
                                                                                                                                                                                                                                                                                                                          94608
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CITY: Emer
STATE: CA
                                                                                                                                                                                                                                                                                          S
                                  RESULT 2
US-08-286-521-12
                                                                                                                                                                                                                                                                                                          COUNTRY:
                                                                                                                                                                                                                                                                  CITY: E
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 3
```

```
ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: INNIS, MICHABL A.
APPLICANT: ZAROR, ISABEL
APPLICANT: CREASEL
APPLICANT: CREASEL
TITLE OF INVENTION: CHIMBRIC MCP AND DAF PROTEINS WITH CELL
TITLE OF INVENTION: SURFACE LOCALIZING DOMAIN
NUMBER OF SEQUENCES: 26
CORRESPONDENCE ADDRESS:
ADDRESSE: CHIRON CORPORATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              100.0%; Score 86; DB 1; Length 17; 100.0%; Pred. No. 1.4e-07; Live 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STREET: INTELLECTUAL PROPERTY - R440, P.O. BOX 8097
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/435,149
FILING DATE: 05-MAY-1995
CLASSIFICATION: 530
PatentIn Release #1.0, Version #1.30B
                              CURRENT APPLICATION DATA: APPLICATION NUMBER: US
```

ö

Gaps

```
ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
                                                                                                                      ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                        Gaps
                                                                                                                      ő
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ;
                                                                          Query Match 100.0%; Score 86; DB 2; Length 17; Best Local Similarity 100.0%; Pred. No. 1.4e-07; Matches 17; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 17;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30B
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/943,682
FLING DATE: 03-0CT-1997
CLASSIFICATION 1435
PRIOR APPLICATION DATE: US 08/438,184
FILING DATE: 09-MAY-1995
APPLICATION NUMBER: US 08/438,184
FILING DATE: 05-AUG-1994
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 100.0%; Score 86; DB 4; I Best Local Similarity 100.0%; Pred. No. 1.4e-07; Matches 17; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                      GENERAL INFORMATION:
APPLICANT: Innis, Michael
APPLICANT: Creasey, Abla
TITLE OF INVENTION: Chimeric Proteins
NUMBER OF SEQUENCES: 37
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME: Savereide, Paul B.
REGISTRATION NUMBER: 36,914
REFERENCE/DOCKET NUMBER: 0990.001
TELEPHONE: 510-601-2585
TELEPRAX: 510-65-3542
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 12, Application PC/TUS9509464 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                   Sequence 12, Application US/08943682
Patent No. 6174721
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Chiron Corporation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: CHIRON CORPORATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 AKLNCRLYRKANKSSKL 17
                                                                                                                                                                                1 AKINCRIYRKANKSSKL 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 17 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 AKLNCRLYRKANKSSKL 17
                                                                                                                                                            1 AKLNCRLYRKANKSSKL 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STREET: 4560 Horton St
CITY: Emeryville
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: amino acid
STRANDEDNESS: single
; TOPOLOGY: linear; MOLECULE TYPE: protein US-08-435-149-8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TOPOLOGY: linear MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               94608
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PCT-US95-09464-12
                                                                                                                                                                                                                                                           RESULT 5
US-08-943-682-12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-08-943-682-12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           g
```

```
Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 17;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STAID.

STAID.

SUDTRY: USA
ZIP: 49008-1699
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.5 inches, 1.44 Mb storage
"...nurper: IBM PC/XYI/AT Compatible
"...nurper: IBM PC/XYI/AT Compatible
                                                                                                                                                                                   MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.30B
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/09464
FILING DATE: 25-JULY-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: YOSHITAKE, SHINJI
APPLICANT: SUZUKI, NOBORU
APPLICANT: SETO, TOSHILO
APPLICANT: MGAOKA, NAOKO
APPLICANT: MIZUI, YOSHIHARU
TITLE OF INVENTION: HUMAN ANTITHROMBIN III MUTANT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         E: FLYNN, THIEL, BOUTELL & TANIS, P.C. 2026 Rambling Road
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     100.0%; Score 86; DB 5; I 100.0%; Pred. No. 1.4e-07;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mismatches
    Chimeric Proteins
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US/08/046,431A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 2, Application US/08046431A Patent No. 5420252
                                                                                                                                                                                                                                                                                                       FILING DATE: 25-JULY-1995
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Savereide, Paul B.
REGISTRATION NUMBER: 36,914
REFERENCE/DOCKET NUMBER: 0990.
TELECOMMUNICATION INFORMATION:
TELEPHONE: 510-601-2545
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE GRARACTERISTICS:
                    NUMBER OF SEQUENCES: 37
CORRESPONDENCE ADDRESS:
CHICO COPPORTION
STREET: 4560 HOTTON St.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LENGTH: 17 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 100.
Best Local Similarity 100.
Matches 17; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 AKLNCRLYRKANKSSKL 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 AKLNCRLYRKANKSSKL 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CURRENT APPLICATION DATA:
APPLICATION NUMBER: US
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TOPOLOGY: linear
MOLECULE TYPE: peptide
                                                                                                                                                                             COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NUMBER OF SEQUENCES: 4
TITLE OF INVENTION:
                                                                                                 Emeryville
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STREET: 2026 Ran
CITY: Kalamazoo
STATE: Michigan
                                                                                                                                                       ZIP: 94608
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ADDRESSEE:
                                                                                                                       CA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PCT-US95-09464-12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-08-046-431A-2
                                                                                                                                       COUNTRY:
                                                                                               CITY: E
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT 7
```

CLASSIFICATION: 435

```
; Sequence 8, Application US/08612986
; Patent No. 5770384
; GENERAL INFORMATION:
; APPLICANT: Elliot J. Androphy
APPLICANT: Dave E. Breiding
; TITLE OF INVENTION: E2 BINDING PROTEINS
; NUMBER OF SEQUENCES: 19
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lahive & Cockfield
STREET: 60 State Street, suite 510
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: ASCII text
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/612,986
FILING DATE:
                                                                                                                                                                                            RESULT 9
US-00-348-817A-6
'Sequence 6, Application US/09348817A
'Patent No. 6191260
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME: Myers, Paul L. REGISTRATION NUMBER: 35,965
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CLASSIFICATION: 800
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/361
FILING DATE: 22 DEC 1994
CLASSIFICATION: 800
ATTORNEY/AGENT INFORMATION:
93.0%;
94.1%;
                                                                                                              157 AKLNCRLYRKANKSSDL 173
Query Match
Best Local Similarity 94.1
Matches 16; Conservative
                                                                                      1 AKLNCRLYRKANKSSKL 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 93.0°
Best Local Similarity 94.1°
Matches 16; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 AKLNCRLYRKANKSSKL 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CITY: Boston
STATE: Massachusetts
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ORGANISM: Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ZIP: 02109-1875
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-09-348-817A-6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STATE: Ma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LENGTH: 465
TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-08-612-986-8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           δŏ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 q
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ó
                                                                                                                                                                                                                                                                                                                                                                                                                                                100.0%; Score 86; DB 1; Length 464; 100.0%; Pred. No. 3.6e-06; tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: HASTINGS, GREGG
APPLICANT: COLEMAN, TIM
APPLICANT: COLEMAN, TIM
APPLICANT: LAWRENCE, DANIEL
TITLE OF INVENTION: BRAIN-ASSOCIATED INHIBITOR OF
TITLE OF INVENTION: TISSUE-TYPE PLASMINOGEN ACTIVATOR
NUMBER OF SEQUENCES: 17
ADDRESSEE: HUMAN GENOME SCIENCES, INC.
STREET: 9410 KEY WEST AVENUE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION NATA:
APPLICATION NUMBER: US/08/948,997
FLING DATE: Oct-10-97
CLASSIFICATION: 435
ATONINEY/AGENT INFORMATION:
NAME: A. ANDERS BROOKES
REGISTRATION NUMBER: 36,373
REGISTRATION NUMBER: 36,373
                                                                                                                                                                        Furuya Case 1286
                                                                                                                                                               REFERENCE/DOCKET NUMBER: Furu
TELECOMMUNICATION INFORMATION:
TELEPHONE: (616) 381-1156
TELEFAX: (616) 381-5465
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-08-948-997-6
; Sequence 6, Application US/08948997
; Patent No. 6008020
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               REFERENCE/DOCKET NUMBER:
TELECOMMUNICATION INFORMATION:
TELEPHONE: (301) 309-8504
TELEFAX: (301) 309-8512
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 465 amino acids
                                                       APPLICATION NUMBER: JP31855
FILING DATE: 22-FEB-1993
ATTORNEY/AGENT INFORMATION:
NAME: Terryence F. Chapman
REGISTRATION NUMBER: 32549
                 APPLICATION NUMBER: JP90488
FILING DATE: 10-APR-1992
                                                                                                                                                                                                                                                                                              LENGTH: 464 amino acids
TYPE: amino acid
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             156 AKLNCRLYRKANKSSKL 172
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 AKLNCRLYRKANKSSKL 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Best Local Similarity 100.
Matches 17; Conservative
                                                                                                                                                                                                                                                                                                                                                          MOLECULE TYPE:
DESCRIPTION: protein
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ZIP: 20850
COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; MOLECULE TYPE: protein US-08-948-997-6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ROCKVILLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                    US-08-046-431A-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ò
```

```
ö
                                                                                                                                                                                                                                                                                             GENERAL INFORMATION:
APPLICANT: Hastings et al.
APPLICANT: Hastings et al.
TITLE OF INVENTION: Activator
TITLE OF INVENTION: Activator
FILE REPERBACE: PF336D1
CURRENT APPLICATION NUMBER: 08/09/348,817A
CURRENT FILING DATE: 1999-07-08
PRIOR APPLICATION NUMBER: 08/948,997
PRIOR PLICATION NUMBER: 60/028,117
PRIOR PLICATION NUMBER: 60/028,117
NUMBER OF SEQ ID NOS: 17
SOFTWARE: Patentin Ver: 2.1
SEQ ID NO 6
                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                  ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             93.0%; Score 80; DB 4; Length 465; 94.1%; Pred. No. 3.2e-05; iive 0; Mismatches 1; Indels
Score 80; DB 3; Length 465;
Pred. No. 3.2e-05;
0; Mismatches 1; Indels
```

```
MOLECULE TYPE: protein
        GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       g
                                                                                                                                                                                                                                           ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ;
0
                                                                                                                                                                                                        Score 46; DB 1; Length 41;
Pred. No. 0.74;
1; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 46; DB 1; Length 41;
Pred. No. 0.74;
1; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Elliot J. Androphy
APPLICANT: Dave E. Breiding
TITLE OF INVENTION: E2 BINDING PROTEINS
UNMBER OF SEQUENCES: 19
CORRESPONDENCE ADDRESS:
ADDRESSEE: Lahive & Cockfield
STREET: 60 State Street, suite 510
REFERENCE/DOCKET NUMBER: NEP-004DV TELECOMMUNICATION: TELEPHONE: (617) 227-7400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SOFTWARE: ASCII text
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/361,806A
FILING DATE: 22 DEC 1994
CLASSIFICATION: 530
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           REFERENCE/DOCKET NUMBER: NEP-004
TELECOMUNICATION INFORMATION:
TELEPHONE: (617) 227-7400
TELEFAX: (617) 227-5941
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARATERISTICS:
LENGTH: 41 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 8, Application PC/TUS9516806A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ZIP: 02109-1875
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                            Sequence 8, Application US/08361806A Patent No. 5792833 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME: Myers, Paul L. REGISTRATION NUMBER: 35,965
                          TELEPHONE: (617) 227-7400
TELEFAX: (617) 227-5941
INFORMATION FOR SEQ ID NO: 8: SEQUENCE CHARACTERISTICS:
LENGTH: 41 aming acids
                                                                                                                                                                                                        53.5%; 72.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        53.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 72.,°,
Best Local Similarity 72.,°,
                                                                                                                                                                                        Query Match
Best Local Similarity 72.7%
                                                                                                     TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-612-986-8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TOPOLOGY: linear
MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STATE: Massachusetts
                                                                                                                                                                                                                                                                                            30 INCRHYRKKNK 40
                                                                                                                                                                                                                                                                        3 LNCRLYRKANK 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          30 INCRHYRKRNK 40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          3 LNCRLYRKANK 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Boston
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT 12
PCT-US95-16806A-8
                                                                                                                                                                                                                                                                                                                                                                        US-08-361-806A-8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-08-361-806A-8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COUNTRY:
                                                                                                                                                                                                                                                                                                          g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         С
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          δ
```

```
Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   No. 57077980 No. 5707798disk of No. 5707798th America
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         .;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 4, Application US/08273669
Patent No. 5707798
GENERAL INFORMATION:
TITLE OF INVENTION: Identification of Ligands by Selective
TITLE OF INVENTION: Amplification of Cells Transfected with
TITLE OF INVENTION: Receptors
NUMBER OF SEQUENCES: 13
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            53.5%; Score 46; DB 5; Length 41; 72.7%; Pred. No. 0.74;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM:

MEDIUW TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/273,669
FILING DATE: 12-JUJ-94
CLASSIFICATION: 435
ATTONNEY/AGENT INFORMATION:
NAME: AGRIS, Cheryl H.
REGISTRATION NUMBER: 34,086
REFERENCE/POCKET NUMBER: 34,086
TELLEPAN: (212) 867-0123
TENDEMATION POR SEO ID NO: 4:
SEQUENCE CHARACTERISTICS:
TENDEMATICE CHARACTERISTICS:
TENDEMH: 20 mmino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1; Mismatches
                    E2 Binding Proteins
                                                                                                                                                    SOFTWARE: ASCII (text)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/16806A
APPLICANT:
TITLE OF INVENTION: E2 Binding Prote
NUMBER OF SEQUENCES: 21
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPACTIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                           PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/361,806
FILLING DATE: 22-DEC-1994
INFORNATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                    December 22, 1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   405 Lexington Avenue
New York
                                                                                                                                                                                                                                                                                                                                                                           H: 41 amino acids amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 72.7'
Matches 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LENGTH: 20 amino acids
TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                  ; TOPOLOGY: linear; MOLECULE TYPE: protein PCT-US95-16806A-8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              30 INCRHYRKKNK 40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                3 LNCRLYRKANK 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         linear
                                                                                                                                                                                                                    FILING DATE: DO CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COUNTRY: U
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                     LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-08-273-669-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STREET:
```

```
ó
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        No. 59121320 No. 5912132disk of No. 5912132th America
                                                                                        0;
                                                                                                                                                                                                                                                                                            Sequence 4, Application US/08954724
Patent No. 5912132
GENERAL INFORMATION:
TITLE OF INVENTION: Identification of Ligands by Selective
TITLE OF INVENTION: Amplification of Cells Transfected with
TITLE OF INVENTION: Receptors
NUMBER OF SEQUENCES: 13
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Brann, Mark R. TITLE OF INVENTION: Identification of Ligands by Selective TITLE OF INVENTION: Amplification of Cells Transfected with
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            50.0%; Score 43; DB 2; Length 20; 53.3%; Pred. No. 1.1;
                                      50.0%; Score 43; DB 1; Length 20; 53.3%; Pred. No. 1.1; tive 3; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/954,724
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CLASSIFICATION:
PRIOR APPLICATION:
PROR APPLICATION DATA:
PRIOR DATE:
PELING DATE: 12-JUL-94
ATTORNEY/AGENT INFORMATION:
NAME: AGRIS, Cheryl H.
REGISTRATION NUMBER: 34,086
REFERENCE/DOCKET NUMBER: 4011.200-US
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEFAX: (212) 867-0123
TELEFAX: (212) 878-9655
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 4, Application US/08965947
Patent No. 5955281
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STREET: 405 Lexington Avenue CITY: New York STATE: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LENGTH: 20 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Best Local Similarity 53.3
Matches 8; Conservative
                                                                                        Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TOPOLOGY: linear MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  3 LNCRLYRKANKSSKL 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             | ||:|| | | :|:
| LYCRIYRVAEKRIKV 15
                                                                                                                                      3 LNCRLYRKANKSSKL 17
                                                                                                                                                                  | ||:|| | :|:
| LYCRIYRVAEKRTKV 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: amino acid
STRANDEDNESS: sir
                                                              Best Local Similarity
Matches 8; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 10174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-08-965-947-4
                                                                                                                                                                                                                                                                            US-08-954-724-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-08-954-724-4
US-08-273-669-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
                                               Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ŏ
                                                                                                                                                                                 g
```

ő

```
CORRESPONDENCE ADDRESS:
ADDRESSEE: No. 59552810 No. 5955281disk of No. 5955281th America
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      .;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     50.0%; Score 43; DB 2; Length 20; 53.3%; Pred. No. 1.1; tive 3; Mismatches 4; Indels
                                                                                                                                                                                                                                     COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PARENTIN Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/965,947
                                                                                                                                                                                                                                                                                                                                                                         CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/273,669
FILING DATE: 12-UUL-94
ATTORNEY/AGENT INFORMATION:
NAME: AGRIS, Cheryl H.
RGGISTRATION NUMBER: 34,086
REFERENCE/DOCKET NUMBER: 4011.200-US
TELECOMMUNICATION INFORMATION:
TELECHONE: (212) 878-9655
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Search completed: December 2, 2002, 10:05:58 Job time: 3.79104 secs
                                                                                   405 Lexington Avenue
TITLE OF INVENTION: Receptors
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 50.0%;
Best Local Similarity 53.3%;
Matches 8; Conservative
                                                                                                                                                                                                COMPUTER READABLE FORM: MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEFAX: (212) 878-965: INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      20 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TOPOLOGY: linear
MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         | ||:|| | |:|:
| LYCRIYRVAEKRIKV 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                3 LNCRLYRKANKSSKL 17
                       NUMBER OF SEQUENCES:
                                                                                                          New York
New York
                                                                                                                                                    USA
                                                                                                                                                                                                                                                                                                                                                         FILING DATE:
                                                                                                                                                    COUNTRY: US
ZIP: 10174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-08-965-947-4
                                                                                     STREET:
```

```
GenCore version 5.1.3
Copyright (c) 1993 - 2002 Compugen Ltd.
```

OM protein - protein search, using sw model

December 2, 2002, 10:00:50; Search time 1.60697 Seconds Run on:

(without alignments)
168.461 Million cell updates/sec

US-09-741-106-12 86 Perfect score:

1 AKLNCRLYRKANKSSKL 17 Sequence:

Scoring table:

BLOSUM62 Gapop 10.0 , Gapext 0.5

102317 seqs, 15924203 residues Searched:

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database :

/cgn2\_6/ptodata/1/pubpaa/US08\_NEW\_PUB.pep:\*
/cgn2\_6/ptodata/1/pubpaa/US08\_NEW\_PUB.pep:\*
/cgn2\_6/ptodata/1/pubpaa/US06\_NEW\_PUB.pep:\*
/cgn2\_6/ptodata/1/pubpaa/US06\_PUBCOMB.pep:\*
/cgn2\_6/ptodata/1/pubpaa/US07\_NEW\_PUB.pep:\*
/cgn2\_6/ptodata/1/pubpaa/US07\_NEW\_PUB.pep:\*
/cgn2\_6/ptodata/1/pubpaa/US08\_PUBCOMB.pep:\*
/cgn2\_6/ptodata/1/pubpaa/US08\_PUBCOMB.pep:\*
/cgn2\_6/ptodata/1/pubpaa/US08\_PUBCOMB.pep:\*
/cgn2\_6/ptodata/1/pubpaa/US08\_PUBCOMB.pep:\*
/cgn2\_6/ptodata/1/pubpaa/US09\_PUBCOMB.pep:\*
/cgn2\_6/ptodata/1/pubpaa/US09\_PUBCOMB.pep:\* /cgn2\_6/ptodata/1/pubpaa/US10\_NEW\_PUB.pep:\*/cgn2\_6/ptodata/1/pubpaa/US10\_PUBCOMB.pep:\*/cgn2\_6/ptodata/1/pubpaa/US60\_NEW\_PUB.pep:\*/cgn2\_6/ptodata/1/pubpaa/US60\_PUBCOMB.pep:\*/cgn2\_6/ptodata/1/pubpaa/US60\_PUBCOMB.pep:\* Published\_Applications\_AA:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

### SUMMARIES

		о¥Р				
Result	·	Query	:			
NO.	score	Match	Match Length DB	DB	ID	Description
1	98	100.0	464	10	US-09-414-834-1	Sequence 1, Appli
7	80	93.0	465	σ	US-09-987-021-6	Seguence 6, Appli
m	80	93.0	465	10	US-09-957-485-6	Sequence 6, Appli
4	41	47.7	14	10	US-09-848-664-1	
S	41	47.7	498	10	US-09-946-239-8	
9	38	44.2	375	6	US-09-841-730-16	_
7	38	44.2	375	σ	US-09-859-211-31	
ω	37	43.0	221	σ	US-10-108-605-297	Sequence 297, App
σ	36.5	42.4	235	10	US-09-864-761-43113	Ч
10	36.5	42.4	475	12	US-10-142-373-2	Sequence 2, Appli
11	36.5	42.4	478	10	US-09-765-111A-27	Sequence 27, Appl
12	36.5	42.4	505	10	US-09-765-111A-16	
13	36.5	. 42.4	206	12	US-10-109-886-6	Sequence 6, Appli
14	36.5	42.4	777	10	US-09-765-111A-2	
15	36.5	42.4		10	US-09-765-111A-23	
16	36.5	42.4		10	US-09-765-111A-4	4, A
17	36.5	42.4		10	US-09-765-111A-6	
18	35	40.7	14	10	US-09-848-664-4	Sequence 4, Appli
19	35	40.7	136	10	US-09-867-550-396	396

Sequence 13, Appl Sequence 13, Appl Sequence 11, Appl Sequence 11, Appl Sequence 12, Appl Sequence 250, Appl Sequence 374, Appl Sequence 37, Appl Sequence 7, Appl Sequence 7, Appl Sequence 2, Appl Sequence 2, Appl Sequence 2, Appl Sequence 2, Appl Sequence 37, Appl Sequence 31, Appl Sequence 31, Appl Sequence 31, Appl Sequence 31, Appl Sequence 31, Appl Sequence 3, Appli Sequence 2, Appli Sequence 3, Appli Sequence 3, Appli Sequence 2, Appli
US-09-815-242-10715 US-09-33-633-23 US-09-76-736-13 US-09-976-736-12 US-09-976-736-12 US-09-976-736-12 US-09-976-736-12 US-09-976-736-12 US-09-764-864-978 US-09-954-197-2 US-09-933-9980-37 US-09-933-9980-37 US-09-957-635-2 US-09-957-635-2 US-09-957-635-2 US-09-958-219-2 US-09-958-219-2 US-09-9815-242-5175 US-09-958-33-9880-38 US-09-956-63-3 US-09-956-63-3 US-09-956-63-3 US-09-956-63-3 US-09-956-63-3 US-09-956-63-3 US-09-956-63-3 US-09-956-63-3 US-09-956-63-3 US-09-956-63-3 US-09-956-63-3 US-09-956-63-3 US-09-966-212-7 US-09-986-212-7 US-09-986-212-7 US-09-986-212-7
11100010111111100011
115 220 220 220 220 220 220 220 220 220 22
0444 0444
ਰਚਾਰਾਚਾਰਾਚਾਰਾਚਾਰਾਚਾਰਾਚਾਰਾ ਜਿੰਨਾ ਨੇ ਨਿੰਨਾ ਨੇ ਨਿੰਨਾ ਨੇ ਨੇ
~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~
01000000000000000000000000000000000000

## ALIGNMENTS

```
APPLICANT: Yepes, et al.
TITLE OF INVENTION: Brain-Associated Inhibitor of Tissue-Type Plasminogen Activato FILE REFERENCE: PF336P2
CURRENT APPLICATION NUMBER: US/09/987,021
CURRENT FILING DATE: 2001-11-13
PRIOR APPLICATION NUMBER: 09/957,485
  Sequence 1. Application US/09414834

Sequence 1. Papplication US/09414834

GENERAL INFORMATION:
SENDIACANT: O'SEMILY, Michael S.
APPLICANT: O'SEMILY, M. Judah
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR INHIBITING ANGIOGENESIS
FILE REFERENCE: 07555.0001
CURRENT APPLICATION NUMBER: US/09/414,834

CURRENT FILING DATE: 1999-10-08
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 1
LENGTH: 464
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      .
0
                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 464;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                          100.0%; Score 86; DB 10; 100.0%; Pred. No. 7.9e-07;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mismatches
                                                                                                                                                                                                                                                                                                                                                            ; OTHER INFORMATION: Antithrombin III
US-09-414-834-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-09-987-021-6
; Sequence 6, Application US/09987021
; Patent No. US20020165147A1
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                156 AKLNCRLYRKANKSSKL 172
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 AKLNCRLYRKANKSSKL 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
                                                                                                                                                                                                                                                                                                                TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity
Matches 17; Conserv
US-09-414-834-1
                                                                                                                                                                                                                                                                                                                                                          FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                QQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Qγ
```

Gaps

```
Sequence 8, Application US/09946239
Patent No. US2020020044945A1
GENERAL INFORMATION:
APPLICANT: Barr, Margaret C.
TITLE OF INVENTION: No. US20020044945A1e1 Feline Immunodeficiency Virus Nucleotide
TITLE OF INVENTION: Polypeptide Sequences
TITLE OF INVENTION: Polypeptide Sequences
CURRENT FILING DATE: 18617.0059
CURRENT FILING DATE: 2001-09-04
PRIOR PRILING DATE: 1999-01-09-04
NUMBER OF SEQ ID NOS: 17
LENGTH: 498
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    OTHER INFORMATION: protein encoded by the gag gene of a recombinant viral OTHER INFORMATION: clone constructed from the genomic DNA of a Pallas's cat felin COTHER INFORMATION: immunodeficiency virus US-09-946-219-8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 16, Application US/09841730
Patent No. US20020157126A1
GENERAL INFORMATION:
APPLICANT: Lee, Se-Jin
APPLICANT: McPherron, Alexandra C.
TITLE OF INVENTION: GROWTH DIFFERENTIATION FACTOR RECEPTORS,
TITLE OF INVENTION: AGONISTS AND ANTAGONISTS THEREOF, AND METHODS OF USING SAME
                                                                                                                                                                                                                                                                                                                                                                                                                       .;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       47.7%; Score 41; DB 10; Length 498; ilarity 61.5%; Pred. No. 19; Conservative 0; Mismatches 5; Indels
                                                                                                                                                                                                                                                                                                                                                                          Length 14;
                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
                                                                                                                                                                                                                                                                                                                                                                                                                     2;
                                                                                                                                                                                                                                                                                                                                                                        Score 41; DB 10;
Pred. No. 0.47;
0; Mismatches 2
                                                                                                                                                                                                                                                                                                           ; OTHER INFORMATION: Xaa is bAla (Beta Alanine)
US-09-848-664-1
FILE REFERENCE: ETH 108
CURRENT APPLICATION NUMBER: US/09/848,664
CURRENT FILING DATE: 2001-05-03,
PRIOR APPLICATION NUMBER: 09/298,084
PRIOR FILING DATE: 1999-04-22
NUMBER OF SEQ ID NOS: 31
SEQ ID NO 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FILE REFERENCE: JHU1470-2
CURRENT APPLICATION NUMBER: US/09/841,730
CURRENT FILING DATE: 2001-04-24
PRIOR APPLICATION NUMBER: 09/626,896
PRIOR FILING DATE: 2000-07-27
                                                                                                                                                                                                                                                                                                                                                                          47.78;
81.8%;
                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 81.0.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               423 NCRAPRKCNKCGK 435
                                                                                                                                                                                                 TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    4 NCRLYRKANKSSK 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 AKLNCRLYRKA 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         4 AKLAARLYRKA 14
                                                                                                                                                                                                                                                                NAME/KEY: MOD_RES
LOCATION: (2)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: PRT
ORGANISM: Unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-09-841-730-16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 5
US-09-946-239-8
                                                                                                                                                                                  LENGTH: 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      δλ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  δλ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    qq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 1, Application US/09848664

Patent No. US20020146414A1

GENERAL INFORMATION:
APPLICANT: Sakiyama-Elbert, Shelly E.
APPLICANT: Hubbell, Jeffrey A.

TITLE OF INVENTION: Controlled Release of No. US20020146414A1-Heparin Binding Growth

TITLE OF INVENTION: Factors from Heparin Containing Matrices
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT 3
US-09-957-485-6
; Sequence 6, Application US/09957485
; Patent No. US2002014316541
; GENERAL INFORMATION:
; APPLICANT: Human Genome Sciences, Inc. et al.
; TITLE OF INVENTION: Brain-Associated Inhibitor of Tissue-Type Plasminogen
; FILE REFERENCE: PF336P1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ;;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      93.0%; Score 80; DB 10; Length 465; 94.1%; Pred. No. 7.5e-06; Live 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 465;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 80; DB 9; Length 405
Pred. No. 7.5e-06;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CURRENT APPLICATION NUMBER: US/09/957,485
CURRENT FILING DATE: 2001-09-21
PRIOR APPLICATION NUMBER: US 09/521,664
PRIOR FILING DATE: 2000-03-08
PRIOR FILING DATE: 1999-03-10
NUMBER OF SEQ ID NOS: 21
SEQ ID NO 6
                  PRIOR APPLICATION NUMBER: 09/722,292
PRIOR FILING DATE: 2000-11-28
PRIOR PELING DATE: 2000-11-28
PRIOR PELING DATE: 2000-11-14
PRIOR FILING DATE: 2000-11-14
PRIOR APPLICATION NUMBER: 09/521,664
PRIOR FILING DATE: 2000-03-08
PRIOR PELING DATE: 1999-07-08
PRIOR FILING DATE: 1999-03-10
PRIOR APPLICATION NUMBER: 60/123,704
PRIOR APPLICATION NUMBER: 60/123,704
PRIOR APPLICATION NUMBER: 60/10
PRIOR APPLICATION NUMBER: 60/10
PRIOR PELING DATE: 1997-10-10
PRIOR FILING DATE: 1997-10-11
NUMBER OF SEQ ID NOS: 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         93.0%;
94.1%;
      PRIOR FILING DATE: 2001-09-21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     157 AKLNCRLYRKANKSSDL 173
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       157 AKLNCRLYRKANKSSDL 173
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 93.0°
Best Local Similarity 94.1
Matches 16; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 AKLNCRLYRKANKSSKL 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 AKLNCRLYRKANKSSKL 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 16; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                       ; ORGANISM: Mus musculus US-09-987-021-6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; ORGANISM: Mus musculus US-09-957-485-6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Best Local Similarity
Matches 16; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LENGTH: 465
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 4
US-09-848-664-1
                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                             SEQ ID NO 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
                                                                                                                                                                                                                                                                                                                                                                                                   LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    qq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ó
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              õ
```

ö

Gaps

```
Score 37; DB 9; Length 221;
Pred. No. 36;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CURRENT APPLICATION NUMBER: US/09/864,761
CURRENT APPLICATION NUMBER: US/09/864,761
CURRENT APPLICATION NUMBER: US/09/864,761
CURRENT APPLICATION NUMBER: US/09/864,761
CURRENT APPLICATION NUMBER: US 60/180,312
PRIOR FILING DATE: 2000-02-04
PRIOR FILING DATE: 2000-05-26
PRIOR FILING DATE: 2000-08-03
PRIOR FILING DATE: 2000-08-03
PRIOR FILING DATE: 2000-09-07
PRIOR PLING DATE: 2000-09-07
PRIOR FILING DATE: 2000-09-07
PRIOR FILING DATE: 2001-01-30
PRIOR FILING DATE: 2001-01-30
PRIOR FILING DATE: 2001-01-30
PRIOR PELING DATE: 2001-01-30
PRIOR PELING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00664
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00665
PRIOR APPLICATION NUMBER: PCT/US01/00667
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         R FILING DATE: 2001-01-30
R APPLICATION NUMBER: PCT/US01/00663
R FILING DATE: 2001-01-30
R APPLICATION NUMBER: PCT/US01/00662
R APPLICATION NUMBER: PCT/US01/00661
R APPLICATION NUMBER: PCT/US01/00661
R APPLICATION NUMBER: PCT/US01/00661
R FILING DATE: 2001-01-30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: PCT/US01/00670
FILING DAFE: 201-01-30
APPLICATION NUMBER: US 60/234,687
FILING DATE: 2000-09-21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 43113, Application US/09864761 Patent No. US20020048763A1
                                                                                                                                                                                                                                                                                                                                                                                                 ; TYPE: PRT
; ORGANISM: Drosophila melanogaster
US-10-108-605-297
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                43.08;
63.68;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Ouery Match
Best Local Similarity 63.6°
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            6 RLYRKANKSSK 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                61 RLYRKKNDNAK 71
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-09-864-761-43113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            δλ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                q
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                        .;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ö
                                                                                                                                                                                                                                                                                                                                                                                           44.2%; Score 38; DB 9; Length 375; 57.1%; Pred. No. 43;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                44.2%; Score 38; DB 9; Length 375; 57.1%; Pred. No. 43;
                                                                                                                                                                                                                                                                                                                                                                                                                                                     3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 31, Application US/09859211
Fatent No. US20020157125A1
GENERAL INFORMATION:
APPLICANT: Lee, Se-Jin
APPLICANT: McPherron, Alexandra C.
TITLE COF INVENTION: GROWTH DIFFERENTIATION FACTOR-8
FILE REFERENCE: 07265/144001
CURRENT APPLICATION UNMERR: US/09/859,211
CURRENT PILING DATE: 2001-05-15
PRIOR RILING DATE: 1997-02-05
PRIOR FILING DATE: 1997-02-05
PRIOR FILING DATE: 1997-02-05
PRIOR APPLICATION NUMBER: 08/847,910
PRIOR FILING DATE: 1997-02-05
PRIOR APPLICATION NUMBER: 08/795,071
PRIOR FILING DATE: 1997-02-05
PRIOR FILING DATE: 1997-02-05
PRIOR FILING DATE: 1997-02-05
PRIOR APPLICATION NUMBER: 08/795,071
PRIOR FILING DATE: 1997-03-05
PRIOR APPLICATION NUMBER: 08/795,071
PRIOR FILING DATE: 1997-03-18
PRIOR FILING DATE: 1997-03-18
PRIOR FILING DATE: 1997-03-18
PRIOR FILING DATE: 1994-03-18
PRIOR FILING DATE: 1994-03-18
PRIOR FILING DATE: 1994-03-18
PRIOR FILING DATE: 1993-03-19
NUMBER OF SEQ ID NOS: 51
SECTION ON AND 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                  3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        3; Mismatches
                 PRIOR FILING DATE: 2000-01-31
PRIOR APPLICATION NUMBER: PCT/US98/15598
PRIOR FILING DATE: 1998-07-28
PRIOR FILING DATE: 1998-07-28
PRIOR FILING DATE: 1997-08-01
NUMBER OF SEQ ID NOS: 29
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 16
LENGTH: 375
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 297, Application US/10108605
Patent No. US20020160934A1
GENERAL INFORMATION:
APPLICANT: Broadus, Julie
APPLICANT: Stam, Lynn
APPLICANT: Bachmann, Jane
PRIOR APPLICATION NUMBER: 09/485,046
                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          4 NCRLYRKANKSSKL 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          40 NACLWRQNNKSSRL 53
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               4 NCRLYRKANKSSKL 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               40 NACLWRQNNKSSRL 53
                                                                                                                                                                                                                                                                                                                                                                                                                        Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Best Local Similarity
Matches 8; Conserv
                                                                                                                                                                                                                                                                                                         ORGANISM: Ovine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: PRT
ORGANISM: Ovine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-10-108-605-297
                                                                                                                                                                                                                                                                                                                                   US-09-841-730-16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-09-859-211-31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQ ID NO 31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-09-859-211-31
                                                                                                                                                                                                                                                                               TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                           Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                             Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Op
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  õ
```

```
APPLICANT: Kamdar, Kim

TITLE OF INVENTION: NUCLEIC ACID SEQUENCES FROM DROSOPHILA MELANOGASTER THAT ENCOD

TITLE OF INVENTION: PROTEINS ESSENTIAL FOR LARVAL VIABILITY AND USES THEREOF
FILE REFERENCE: 31133

CURRENT APPLICATION NUMBER: US/10/108,605

CURRENT FILING DATE: 2002-03-27

PRIOR APPLICATION NUMBER: US 69/761,142

PRIOR APPLICATION NUMBER: US 60/176,418

PRIOR PILING DATE: 2000-01-14

PRIOR FILING DATE: 2000-01-14

SEQ ID NOS: 361

SEQ ID NOS: 361

SEQ ID NO 297

LENGTH: 221
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Penn, Sharron G.
APPLICANT: Rank, David R.
APPLICANT: Hanzel, David K.
APPLICANT: Chen, Wensheng
TITLE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ..
0
```

```
US-09-765-111A-16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-09-765-111A-16
                                                                                                                                                                                                                                                                                     US-09-765-111A-27
                                                                                                                                                                                                                   LENGIH: 478
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT 13
US-10-109-886-6
                                                                                                                                                                                                                                         TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LENGIH: 50
TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 12
                                                                                                                                                                                                                                                                                                                                                                                                                                    δλ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           q
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      δλ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: EVANS, Ronald
APPLICANT: FORMATION:
APPLICANT: FORMATION:
APPLICANT: FORMATION:
APPLICANT: FORMATION:
APPLICANT: FORMATION: BAITY
TITLE OF INVENTION: MODILATOR GAMMA,
TITLE OF INVENTION: AND METHODS FOR THE USE THEREOF
FILE REFERENCE: SALK140-
CURRENT APPLICATION NUMBER: US/10/142,373
CURRENT FILING DATE: 2002-05-08
PRIOR FILING DATE: 2002-05-08
PRIOR FILING DATE: 2001-02-16
PRIOR PLICATION NUMBER: US/99/788,070
PRIOR PLICATION NUMBER: US/99/788,070
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Ĥ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 36.5; DB 10; Length 235; Pred. No. 47;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      42.4%; Score 36.5; DB 12; Length 475; 58.3%; Pred. No. 97;
                                                                                                                                                                                                                                  FEATURE:

OTHER INFORMATION: MAP TO ACO04613.1

OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 1

OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 1.1

OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 1.3

OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 1.3

OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 1.1

OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 1.0

OTHER INFORMATION: STATEMENT AND ADULT LIVER, SIGNAL = 1.0

OTHER INFORMATION: SWISSPROT HIT: Q61200, EVALUE 1.00e-129

US-09-864-761-43113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 27, Application US/09765111A
PREFERT NO. US20020106796A1
GENERAL INFORMATION:
APPLICANT: Fletcher, Jonathan A.
APPLICANT: Fletcher, Jonathan A.
TITLE OF INVENTION: PAX8-PPARgamma NUCLEIC ACID MOLECULES
TITLE OF INVENTION: AND POLYPEPTIDES AND USES THEREOF
FILE REFERENCE: B0801_71.96/ERP/MAT
                   PRIOR FILING DATE: 2000-06-30
PRIOR APPLICATION NUMBER: US 09/774,203
PRIOR FILING DATE: 2001-01-29
NUMBER OF SEQ ID NOS: 49117
SOFTWARE: Annomax Sequence Listing Engine vers. 1.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          4; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     4; Mismatches
PRIOR APPLICATION NUMBER: US 09/608,408
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 2, Application US/10142373 Patent No. US20020137665A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              42.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRIOR FILING DATE: 1999-02-22
NUMBER OF SEQ ID NOS: 7
SOFTWARE: Patentin version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 50.000
Best Local 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Best_Local Similarity 58.3
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     169 NCRIEYEKVDKATK 182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         4 NCRL-YRKANKSSK 16
                                                                                                                                                                                          TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ||||:::|: ||
148 LNCRIHKKSRNK 159
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; ORGANISM: Mus Musculus
US-10-142-373-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 3 LNCRLYRKA-NK 13
                                                                                                                                         SEQ ID NO 43113
LENGTH: 235
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT 11
US-09-765-111A-27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQ ID NO 2
LENGTH: 475
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-10-142-373-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ŏ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           δλ
```

```
Sequence 6, Application US/10109886

Patent No. US20020119499A1

GENERAL INFORMATION:

APPLICANT: TANABE SEIYAKU CO. LTD.

APPLICANT: TANIGUCHI, TOMOYASU.

APPLICANT: TANIGUCHI, TOMOYASU.

TITLE OF INVENTION: MATAGONIST TO PPAR

FILE REFERENCE: TANIGUCHI=6

CURRENT APPLICATION NUMBER: US/10/109,886

CURRENT PELLING DATE: 2002-04-01

PRIOR FILING DATE: 2002-04-01

PRIOR FILING DATE: 1998-08-24

PRIOR FILING DATE: 1998-08-24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                      1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 505;
                                                                                                                                                                                                                                                                                                           Length 478;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; Sequence 16 Application US/09765111A
; Patent No. US2002010696A1
; GENERAL INFORMATION:
APPLICANT: Fletcher, Jonathan A.
APPLICANT: Fletcher, Jonathan A.
TITLE OF INVENTION: PAX8 PPARGamma NUCLEIC ACID MOLECULES
TITLE OF INVENTION: AND POLYPEPTIDES AND USES THEREOF
FILE REFERENCE: B0801/7196/ERP/MAT
CURRENT APPLICATION NUMBER: US/09/765,111A
CURRENT FILING DATE: 2001-01-18
; PRIOR RPLING DATE: 2000-01-20
; PRIOR PLING DATE: 2000-01-18
; PRIOR PLING DATE: 2000-01-18
; NUMBER OF SEQ ID NOS: 47
; NUMBER OF SEQ ID NOS: 47
; SOFTWARE: EstSEQ for Windows Version 3.0
; SEQ ID NO 16
; SEQ ID NO 16
; LENGTH: 505
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels
                                                                                                                                                                                                                                                                                                                                                        Indels
                                                                                                                                                                                                                                                                                                           Score 36.5; DB 10;
Pred. No. 98;
4; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  42.4%; Score 36.5; DB 10; 58.3%; Pred. No. 1e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               4; Mismatches
CURRENT APPLICATION NUMBER: US/09/765,111A
CURRENT FILING DATE: 2001-01-18
PRIOR PELICATION NUMBER: US 60/17/109
PRIOR FILING DATE: 2000-01-20
PRIOR FILING DATE: 2000-08-14
NUMBER OF SEQ ID NOS: 47
SEQ ID NO 27
                                                                                                                                                                                                                                                                                                              42.4%;
58.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 58.3.
                                                                                                                                                                                                                                                                                                           Query Match 42.4
Best Local Similarity 58.3
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  178 LNCRIHKKSRNK 189
                                                                                                                                                                                                                                              ORGANISM: Homo Sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                            150 LNCRIHKKSRNK 161
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ORGANISM: Homo Sapiens
                                                                                                                                                                                                                                                                                                                                                                                                 3 LNCRLYRKA-NK 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       3 LNCRLYRKA-NK 13
```

1;

```
ï
                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                           1;
                                                                                                                                                                                                                                                                         Query Match 42.4%; Score 36.5; DB 12; Length 506; Best Local Similarity 58.3%; Pred. No. 1e+02; Matches 7; Conservative 4; Mismatches 0; Indels 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 42.4%; Score 36.5; DB 10; Length 777; Best Local Similarity 58.3%; Pred. No. 1.6e+02; Matches 7; Conservative 4; Mismatches 0; Indels 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 2, Application US/09765111A

Petent No. US20020106796A1

GENERAL INFORMATION:
APPLICANT: Fletcher, Jonathan A.
APPLICANT: Fletcher, Jonathan A.
TITLE OF INVENTION: PAX8-PPRRgamma NUCLEIC ACID MOLECULES
TITLE OF INVENTION: DAX8-PPRRGATIONS AND USES THEREOF
FILE REFERENCE: B0801/7196/FRP/MAT
CURRENT APPLICATION NUMBER: US/09/765,111A
CURRENT FILING DATE: 2001-01-18
PRIOR PILICATION NUMBER: US 60/17,109
PRIOR APPLICATION NUMBER: US 60/17,109
PRIOR PPLICATION NUMBER: US 60/225,079
PRIOR APPLICATION NUMBER: 2000-01-20
PRIOR FILING DATE: 2000-08-14
NUMBER OF SEQ ID NOS: 47
SOFTWARE: FRASEQ for Windows Version 3.0
SEQ ID NO 2
LENGTH: 777
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 15
US-09-765-111A-23
; Sequence 23, Application US/09765111A
; Patent No. US20020106796A1
; GENERAL INFORMATION:
APPLICANT: Fletcher, Jonathan A.
APPLICANT: Fletcher, Jonathan A.
TITLE OF INVENTION: PAX8-PPARGamma NUCLEIC ACID MOLECULES
TITLE OF INVENTION: PAX8-PPARGamma NUCLEIC ACID MOLECULES
; TITLE OF INVENTION: PAX8-PPARGamma NUCLEIC ACID MOLECULES
; TITLE OF INVENTION: PAX8-PPARGAMAT
CURRENT APPLICATION NUMBER: US/09/765,111A
; CURRENT FILING DATE: 2000-01-20
; PRIOR FILING DATE: 2000-01-3
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NOS: 47
; SEQ ID NO 23
; TYPE: PRT
PRIOR APPLICATION NUMBER: JP231084/1997
PRIOR FILING DATE: 1997-08-27
NUMBER OF SEQ ID NOS: 10
SOFTWARE: Patentin version 3.0
SEQ ID NO 6
                                                                                                                                                              TYPE: PRT; ORGANISM: Homo sapiens
US-10-109-886-6
                                                                                                                                                                                                                                                                                                                                                                                                                         ||||:::|: ||
| 178 LNCRIHKKSRNK 189
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: PRT
ORGANISM: Homo Sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ||||:::|: ||
450 LNCRIHKKSRNK 461
                                                                                                                                                                                                                                                                                                                                                                                      3 LNCRLYRKA-NK 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 3 LNCRLYRKA-NK 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT 14
US-09-765-111A-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-09-765-111A-2
                                                                                                                                       LENGTH: 506
                                                                                                                                                                                                                                                                                                                                                                                            δ
                                                                                                                                                                                                                                                                                                                                                                                                                                          g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               qq
```

```
; ORGANISM: Homo Sapiens
US-09-765-111A-23
Usery Match

Query Match

Best Local Similarity 58.3%; Pred. No. 1.7e+02;

Matches 7; Conservative 4; Mismatches 0; Indels 1; Gaps 1;

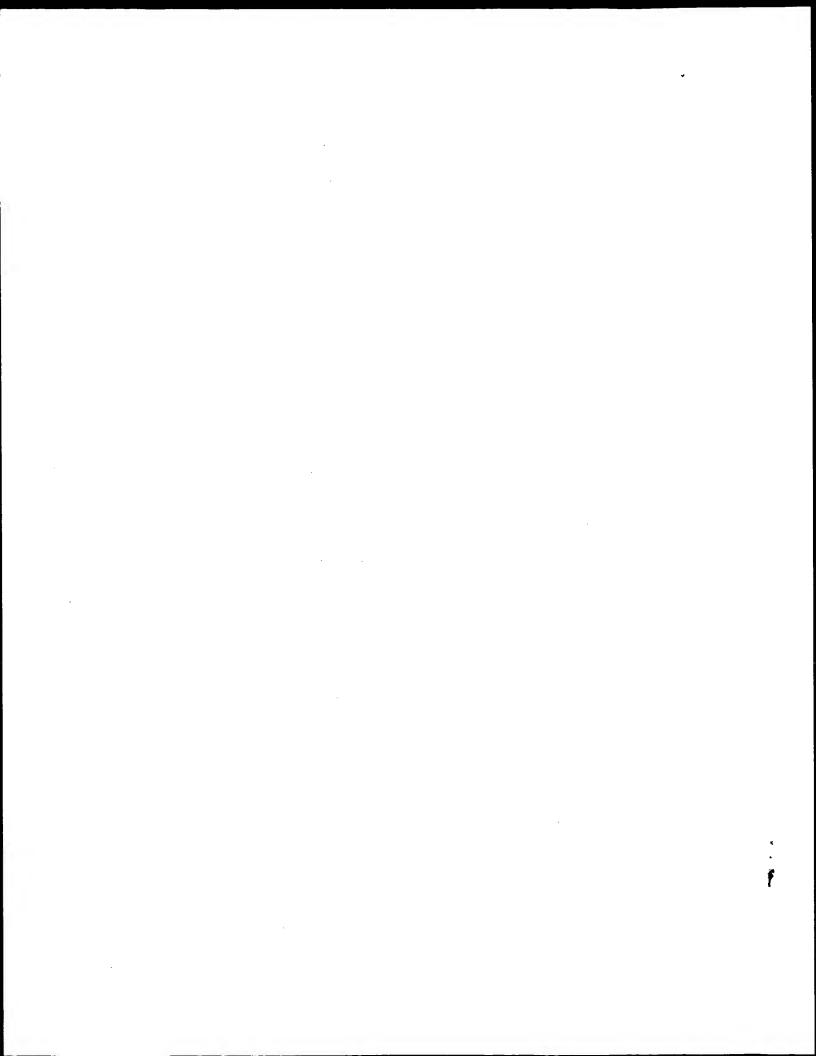
Qy 3 LNCRLYRKA-NK 13

| | | | | | | | | | | | |

Db 484 LNCRIHKKSRNK 495

Search completed: December 2, 2002, 10:05:18

Job time: 2.60697 secs
```



GenCore version 5.1.3 Copyright (c) 1993 - 2002 Compugen Ltd.

protein search, using sw model OM protein

2, 2002, 10:00:35; Search time 3.04478 Seconds December Run on:

(without alignments) 536.751 Million cell updates/sec

1 AKLNCRLYRKANKSSKL 17 US-09-741-106-12 86 Title: Perfect score:

Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

283224 seqs, 96134422 residues Searched:

Total number of hits satisfying chosen parameters:

length: 0 length: 2000000000 Minimum DB Maximum DB

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

PIR\_73:\* Database

1: pirl:\* 2: pir2:\* 3: pir3:\* 4: pir4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

		dР			SUMMARIES	
Result No.	Score	Query	Length	DB	ID	Description
1	98	100.0	464	-	XHHU3	aptithrombin III p
7	82	95.3	431	Н	JX0364	antithrombin III -
٣	82	95.3	433	~	A61435	antithrombin III -
4	82	95.3	465	Н	828219	
Ŋ	80	93.0	465	~	159611	antithrombin III -
9	43	50.0	2010	7	B71616	_
7	42	48.8	407	~	A69989	×
8	41	47.7	285	7	D83380	hypothetical prote
6	41	47.7	531	7	JT0531	muscarinic acetylc
10	41	47.7	532	7	JT0530	muscarinic acetylc
11	41	47.7	664	7	T12988	
12	40	46.5	244	7	D97281	pseudouridylate sv
13	40	46.5	318	Н	YXSAT3	thymidylate syntha
14	40	46.5	623	~	E64201	transport ATP-bind
15	40	46.5	2357	7	A59249	class VII unconven
16	39	45.3	285	7	E69905	transcription requ
17	39	45.3	319	7	T48504	hypothetical prote
18	39	45.3	514	7	A49838	U
19	39	45.3	514	~	AF1988	
	39	45.3	655	7	AI2556	
21	39	45.3	716	7	G44490	
22	39	45.3	943	7	G81070	lactoferrin-bindin
23	39	45.3	944	7	C81798	lactoferrin bindin
24	39	45.3	1700	7	S08167	Balbiani ring 3 pr
25	39	45.3	2067	7	A42854	spindle
26	38	44.2	134	7	JC6091	kinetoplast DNA-as
27	38		173	~	A72612	hypothetical prote
28	38	44.2	257	7	E84107	10
58	38	44.2	301	~	F82287	U

hypothetical prote	hypothetical prote	UDP-glucose 6-dehv	hypothetical prote	nicotinic acetylch	protein W09G3.4 (i	structural protein	type I transmembra	hyaluronan recepto	probable DNA-direc	hypothetical prote	G surface protein	ribosomal protein	rubrervthrin PAB05	probable orotate p	two-component resp
T20208	T29703	E71638	S50755	ACFFNN	C87992	S33316	A45705	JC5016	T28197	T41267	A23475	F69056	D75136	A81441	B84078
~	7	7	7	Н	7	ď	N	7	7	7	~	7	7	7	7
310	402	434	473	521	547	681	681	725	1079	1647	2718	134	175	202	241
44.2	44.2	44.2	44.2	44.2	44.2	44.2	44.2	44.2	44.2	44.2	44.2	43.0	43.0	43.0	43.0
38	38	38	38	38	38	38	38	38	38	38	38	37	37	37	37
30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45

_	
H	
₽	ç
₽	Ξ
Ñ	
띮	5

antithrombin III precursor [validated] - human

C;Species: Homo sapiens (man)
C;Date: 05-Apr-1983 #sequence\_revision 05-Apr-1983 #text\_change 08-Dec-2000
C;Accession: A49494; A93453; A93431; A33305; A34445; A34190; S02530; S63600;
R;Olds, R.J.; Lane, D.A.; Chowdhury, V.; De Stefano, V.; Leone, G.; Thein, S.L.
Biochemistry 32, 4216-4224, 1993
A;Title: Complete nucleotide sequence of the antithrombin gene: evidence for homologo
A;Reference number: A49494; MUID:93237227; PMID:8476848
A;Molecule type: DNA
A;Residues: 1-464 <OLD>
A;Cossion: A49494
A;Molecule type: DNA
A;Residues: 1-464 <OLD>
A;Coss-references: EMBL:X68793; NID:928906; PIDN:CAA48690.1; PID:928907
A;Coss-references: EMBL:X68793; NID:928906; PIDN:CAA48690.1; NCBIP:130248)
R;Bock, S.C.; Wion, K.L.; Vehar, G.A.; Lawn, R.M.
Nucleic Acids Res. 10, 8113-8125, 1982
A;Title: Cloning and expression of the cDNA for human antithrombin III.
A;Reference number: A93453; MUID:83143280; PMID:6298709

A; Residues: 1-464 <BOCIS
A; Residues: 1-464 <BOCIS
A; Residues: 1-464 <BOCIS
A; Residues: 1-464 <BOCIS
A; Cross-references: (B:1.00190; GB:J00102; GB:J00104; NID:g179128; PIDN:AAB
A; Cross-references: (B:1.00190; GB:J00102; GB:J00104; NID:g179128; PIDN:AAB
A; Title: Isolation and sequence characterization of a cDNA clone of human antithrombi
A; Reference number: A93943; MUD:83169777; PMID:6572945
A; Accession: A93943
A; Molecule type: mRNA
A; Residues: 1-464 <CHA>
A; Cross-references: GB:L00190; GB:J00102; GB:J00104; NID:g179128; PIDN:AAB
B; Prochownik, E.V.; Markham, A.F.; Orkin, S.H.
J; Biol. Chem. 258, 8389-8394, 1983
A; Title: Isolation of a cDNA clone for human antithrombin III.
A; Reference number: A92431
A; Residues: 42-96, R, 98-464 <PRO>
A; Residues: 42-96, R, 98-464 <PRO>
A; Residues: 42-96, R, 98-464 <PRO>
A; Note: the authors translated the codon GAC for residue 206 as Asn, GCC for residue
B; Chang, J.Y.
J; Biol. Chem. 264, 3111-3115, 1989
A; Title: Binding of heparin to human antithrombin III activates selective chemical mo

A;Reference number: A33305; MUID:89123426; PMID:2492530
A;Accession: A33305
A;Molecule type: protein
A;Molecule type: protein
A;Residues: 90-105;124-143;147-161;165-171;268-273;381-402;446-457 <CH2>
B;Petersen, T.E.; Dudek-Wojciechowska, G.; Sottrup-Jensen, L.; Magnusson, S. in The Physiological Inhibitors of Blood Coagulation and Fibrinolysis, Collen, D., Wi A;Title: Primary structure of antithrombin-III (heparin cofactor). Partial homology b A;Accession: A94445

```
A; Molecule type: protein
A; Residues: 53-61 cROR>
A; Rees variant form Rouen-IV, 56-Cys, was also sequenced
A; Note: variant form Rouen-IV, 56-Cys, Krawczak, M.; Melissari, E.; Lindo, V.; Mof
B; Grundy, C.B.; Thomas, F.; Millar, D.S.; Krawczak, M.; Melissari, E.; Lindo, V.; Mof
Blood 78, 1027-1032, 1991
A; Reference number: S10716; MUID:90306344; PMID:2365065
A; Accession: S10716
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A; Status: translated from GB/EMBL/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        156 AKLNCRLYRKANKSSKL 172
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 AKLNCRLYRKANKSSKL 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          17;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Gene: GDB: AT3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      C; Function:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       q
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A; Molecule type: protein
A; Residues: 53-68, QE',71-78, C',80-135 < KOI>
A; Residues: 53-68, QE',71-78, C', 80-135 < KOI>
A; Note: variant Toyama with a substitution of Cys for Arg-79 and consequently cannot bin R; Bock, S.C.; Marrinan, J.A.; Radziejewska, E.
Biochemistry 27, 6171-6178, 1988
A; Title: Antithrombin III Utah: proline-407 to leucine mutation in a highly conserved re A; Reference number: 152399; MUID:89050967; PMID:3191114
A; Note: a published erratum appears in Biochemistry 28, 3628 1989
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A Status: preliminary
A Modecule type: protein
A Modela Modecule type: protein
A Modela Modecule type: protein and the protein polymorphism 5' to the human antithrow
A Modecule mumber: 137191; MUID:84169500; PMID:6672771
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Molecule type: protein
A; Residues: 33-39, X', 41-42; 67-77, 'XX', 80-88, 'X', 90-92; 137-142; 189-202; 210-214, 'X'; 265-2
R; Chang, W.S.W.; Wardell, M.R.; Lomas, D.A.; Carrell, R.W.
Biochem J. 314, 647-653, 1996
A; Title: Probing serpin reactive-loop conformations by proteolytic cleavage.
A; Reference number: S63599; MUID:96239126; PMID:8670081
                                               A; Residues: 33-68, Og', 71-242; 243-245, 248-250; 254-464 <PET>
A; Note: carbohydrate-binding site and disulfide bonds
R; Zettlmeissl. G; Conradt, H.S.; Nimtz, M.; Karges, H.E.
J. Biol. Chem. 264, 21159-21159, 1989
A; Title: Characterization of recombinant human antithrombin III synthesized in Chinese
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            R;Liu, C.S.; Chang, J.Y.
Eur. J. Biochem. 167, 247-252, 1987
A;Title: Probing the heparin-binding domain of human antithrombin III with V8 protease.
A;Reference number: S02530; MUID:87304255; PMID:3305015
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Molecule type: DNA
A; Residues: 1-14 GROZZ-X
A; Cross-references: EMBL:X00237; NID:928917; PIDN:CAA25059.1; PID:928918; EMBL:X00238;
A; Kroide, T.; Odani, S.; Takahashi, K.; Ono, T.; Sakuragawa, N.
Proc. Natl. Acad. Sci. U.S.A. 81, 289-229; 1984
A; Title: A Antithrombin III Toyama: replacement of arginine-47 by cysteine in hereditary
A; Reference number: A29371; MUID:84119472; PMID:6582486
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           R;Borg, J.Y.; Brennan, S.O.; Carrell, R.W.; George, P.; Perry, D.J.; Shaw, J. FEBS Lett. 266, 163-166, 1990
A;Title-Antithrombin rouen-IV 24 Arg->Cys. The amino-terminal contribution to heparin
                                                                                                                                                                                                                                                                                                                                                  A;Molecule type: protein
A;Residues: 33-39 <ZET>
A;Experimental source: recombinant protein from Chinese hamster ovary (CHO) cells
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Cross-references: GB:M21644; NID:g179148; PIDN:AAA51794.1; PID:g179151
A;Accession: 165278
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A; Cross-references: GB: M21645; NID: 9179149; PIDN: AAA51795.1; PID: 9179152
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Cross-references: GB:M21642; NID:g179159; PIDN:AAA51796.1; PID:g179161
A;Note: mutant Utah
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Cross-references: GB: M21643; NID: g179147; PIDN: AAA51793.1; PID: g457132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Status: translation not shown; translated from GB/EMBL/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Accession: 165277
A;Status: translation not shown; translated from GB/EMBL/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Status: translation not shown; translated from GB/EMBL/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Status: translation not shown; translated from GB/EMBL/DDBJ
                                                                                                                                                                                                                                                                    A; Reference number: A34190; MUID:90078215; PMID:2592368
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A; Status: preliminary; translated from GB/EMBL/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Residues: 1-438, 'L', 440-464 <BOC6>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Molecule type: DNA
A; Residues: 137-208 <BOC3>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A; Molecule type: DNA
A; Residues: 137-254 <BOC4>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A; Molecule type: DNA
A; Residues: 407-464 <BOC5>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Accession: I65279
                                                                                                                                                                                                                                                                                                                A; Accession: A34190
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Accession: S02530
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A; Accession: S63600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A; Accession: I37191
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Accession: A29371
```

```
A; Residues: 79, CLGTVQGOFPLCYHFLSAPGRFQE' < DALL>
A; Residues: 79, CLGTVQGOFPLCYHFLSAPGRFQE' < DALL>
A; Residues: 79, CLGTVQGOFPLCYHFLSAPGRFQE' < DALL>
A; Cross-references: GB:S43612; NID:9254806; PIDN:AAB23132.1; PID:9254807
A; Accession: 18129
A; Status: translated from GB/EMBL/DDBJ
A; Status: translated from GB/EMBL/DDBJ
A; Molecule type: DNA
A; Redidues: 401, KRHFLK' < DAL2>
A; Cross-references: GB:S43621; NID:9254810; PIDN:AAB23134.1; PID:9254811
A; Note: Irameshiff mutant, patient;
A; Note: Irameshiff mutant, patient;
A; Note: Irameshiff mutant, patient;
A; Note: Translating mutant, patient;
A; FEBS Lett. 126, 257-260, 1981
A; Title: The site in human antithrombin for functional proteolytic cleavage by human A; Reference number: A91287; MuID:81212814; PMID:7238875
A; Contents: annotation; inhibitory site
A; FBlackburn, M. N.; Smith, R. L.; Carson, J.; Sibley, C.C.
J; Blol. Chem. 259, 939-941, 1984
A; Title: The heparin-binding site of antithrombin III. Identification of a critical the A; Reference number: A9248; MuID:84111578; PMID:6593405
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Molecule type: DNA
A; Residues: 271-276, VVFSIYDVPGRQVPLSARG' <GR2>
A; Residues: 271-276, VVFSIYDVPGRQVPLSARG' <GR2>
A; Cross-references: GB: 849759; NID: 9233570; PIDN: AAB19468.1; PID: 9233571
A; Cross-references: GB: 849759; NID: 9233570; PIDN: AB19468.1; PID: 9233571
A; Cross-references: GB: 849759; NID: 923570; NID: 9233571
A; Note: sequence extracted from NCB1 backbone (NCBIN: 49759, NCBIP: 49760)
A; Note: different frameshift mutations at an identical site in unrelated patients sug R; Daly, M.; Perry, D.J.; Harper, P.L.; Daly, H.M.; Roques, A.W.; Carrell, R.W.
Thromb. Haemost. 67, 521-525, 1992
A; Pitle: Insertions/deletions in the antithrombin gene: 3 mutations associated with n A; Accession: I59610; MID: 92390894; PMID: 1325679
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A) Description: in blood plasma inhibits thrombin and activated coagulation factor X, A) Description: in blood plasma inhibits thrombin and activated coagulation factor X, C) Superfamily: antithrombin III
C) Superfamily: actute phase; glycoprotein; heparin binding; plasma; serine proteinase inh E; 13.7 Domain: signal sequence #status predicted <SIG> F; 33.464/Product: antithrombin III #status experimental <MAT> F; 40.160, 53.127, 279-462/Disulfide bonds: #status experimental F; 41.187, 224/Binding site: heparin (Trp) #status experimental F; 128, 167, 187, 224/Binding site: carbohydrate (Asn) (covalent) #status experimental F; 425-426/Cleavage site: Arg-Ser (thrombin) #status experimental F; 425/Inhibitory site: Arg (thrombin, coagulation factor Xa) #status experimental
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                     A;Molecule type: DNA
A;Residues: 271-276,'GRVQHL' <GR1>
A;Cross-references: GB:S49757; NID:g233568; PIDN:AAB19467.1; PID:g233569
A;Cross-references: GB:S49757; NID:g233569
A;Experimental source: antithrombin III deficiency patient 1
A;Note: sequence extracted from NCBI backbone (NCBIN:49757, NCBIP:49758)
A;Accession: B44935
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          100.0%; Score 86; DB 1; Length 464; 100.0%; Pred. No. 5.8e-07;
A;Title: Recurrent deletion in the human antithrombin III gene. A;Reference number: A44935; MUID:91329813; PMID:1868237 A;Accession: A44935
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A,Map position: 1q23-1q25.1
A;Introns: 14/2; 136/3; 208/3; 254/3; 385/1; 406/3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Contents: annotation; heparin-binding site C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A; Cross-references: GDB:119024; OMIM:107300
```

```
phosphatase (acid phosphatase family) PFB0380c - malaria parasite (Plasmodium falcipa C,Species: Plasmodium falciparum C,Species: Plasmodium falciparum C,Species: Plasmodium falciparum C,Species: Plasmodium falciparum C,Species: 13-Nov-1998 #sequence_revision 13-Nov-1998 #text_change 21-Jul-2000 C;Accession: B71616 R;Gardner, M.J.; Tettelin, H.; Carucci, D.J.; Cummings, L.M.; Aravind, L.; Koonin, E.; Fertea, M.; Salzberg, S.; Zhou, L.; Sutton, G.G.; Clayton, R.; White, O.; Smith, H Science 282, 1126-1132, 1998 A;Title: Chromosome 2 sequence of the human malaria parasite Plasmodium falciparum. A;Reference number: A71600; MUID:99021743; PMID:9804551 A;Accession: B71616 A;Status: preliminary; nucleic acid sequence not shown; translation not shown A;Rolecule type: DNA A;Rosidues: 1-2010 cGAR> A;Cross-references: GB:AE001391; GB:AE001362; NID:93845168; PIDN:AAC71865.1; PID:9384 A;Experimental source: clone 3D?
                    A.Wolecule type: mRNA
A.Residues: 1-465 <NLE>
A.Cross-references: EMBL:X68287; NID:g1194; PIDN:CAA48347.1; PID:g1195
A.Cross-references: EMBL:X68287; NID:g1194; PIDN:CAA48347.1; PID:g1195
G.Function: Inhibits in blood plasma thrombin and activated coagulation factor X, C.Superfamily: antithrombin III
C.Keywords: glycoprotein; plasma; serine proteinase inhibitor
C.Keywords: glycoprotein; plasma; serine proteinase inhibitor
F.1-32/Domain: signal sequence #status predicted <SIG>
F.33-465/Product: antithrombin III #status predicted <MAT>
F.129,168,188,225/Binding site: carbohydrate (Asn) (covalent) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                            ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    mouse antithrombin III
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        C;Species: Mus sp. (mouse)
C;Date: 02-Aug-1996 #sequence_revision 02-Aug-1996 #text_change 16-Jul-1999
C;Accession: 155611
R;Wu, J.K.; Sheffield, W.P.; Blajchman, M.A.
Thromb. Haemost. 68, 291-296, 1992
A;Title: Molscular cloning and cell-free expression of mouse antithrombin II
A;Reference number: 159611; MUID:93069082; PMID:1440494
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Cross-references: GB:S47225; NID:9258958; PIDN:AAB23965.1; PID:9258959
C;Superfamily: antithrombin III
                                                                                                                                                                                                                                                                                                                                                                                                                                                            ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       50.0%; Score 43; DB 2; Length 2010; Sonsetvative 2; Mismathhan
                                                                                                                                                                                                                                                                                                                                                                                         Length 465;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           93.0%; Score 80; DB 2; Length 465; 94.1%; Pred. No. 6.3e-06;
                                                                                                                                                                                                                                                                                                                                                                                     Score 82; DB 1; Length 465
Pred. No. 2.8e-06;
1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Status: preliminary; translated from GB/EMBL/DDBJ A;Molecule type: mRNA A;Residues: 1-465 <RES>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                         95.3%;
94.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       157 AKLNCRLYRKANKSSEL 173
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 157 AKLNCRLYRKANKSSDL 173
                                                                                                                                                                                                                                                                                                                                                                                     Query Match 95.3%
Best Local Similarity 94.1%
Matches 16; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 AKLNCRLYRKANKSSKL 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Local Similarity 94.1
nes 16; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 AKLNCRLYRKANKSSKL 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  3 LNCRLYRKANKSSK 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         antithrombin III - mouse
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity
Matches 8; Conserva
A; Accession: S28219
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A; Gene: PFB0380c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ô
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    δy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              q
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  δ
                                                                                                                                                                                                                                                                                                                               A. Accession: JX0364
A. Molecule type: protein
C. Function:
A. Description: inhibits in blood plasma thrombin and activated coagulation factor X, eit C. Superfamily: antithrombin III
C. Superfamily: antithrombin; hepatic bredicted
F. 378-382. Region: hinge #status predicted
F. 91-129, 22-96, 248-431. Prisulfide bonds: #status predicted
F. 934. Inhibitory site: Arg (thrombin) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A Description: inhibits in blood plasma thrombin and activated coagulation factor X, eit C; Superfamily: antithrombin III
C; Superfamily: antithrombin III
C; Superfamily: antithrombin III
C; Superfamily: antithrombin III
C; Steywords: antithrompin III
F; 9-129, 22-96, 248-431/Disulfide bonds: #status predicted
F; 97, 136, 156, 193/Binding site: carbohydrate (Asn) (covalent) #status experimental
F; 394/Inhibitory site: Arg (thrombin) #status experimental
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A; Title: The complete amino acid sequence of bovine antithrombin (ATIII).
A; Reference number: A61435; MUID:92029517; PMID:1930634
A; Accession: A61435
A; Molecule type: protein
A; Residues: 1-433 < MED:
C; Comment: This serpin inhibits thrombin and other clotting factors in the presence of C; Function:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
                                                                      antithrombin III - pig
C;Species: Sus scrofa domestica (domestic pig)
C;Species: Sus Scrofa domestica (domestic pig)
C;Accession: J0-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999
C;Accession: J0564
R;Tokunaga, F: Goto, T: Wakabayashi, S.; Koide, T.
J: Biochem: 116, 1170, 1994
A;Title: Amino acid sequence of porcine antithrombin III.
A;Reference number: JX0364; MUID:95204393; PMID:7896748
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Ļ.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         C;Species: Bos primigenius taurus (cattle)
C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999
C;Accession: A61435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    antithrombin III precursor - sheep
C;Species: Ovis orientalis aries, Ovis ammon aries (domestic sheep)
C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       R;Mejdoub, H.; Le Ret, M.; Boulanger, Y.; Maman, M.; Choay, J.; Reinbolt, J. Protein Chem. 10, 205-212, 1991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               C, Accession: S28219
R; Niessen, R.W.L.M.; Sturk, A.; Hordijk, P.L.; Michiels, F.; Peters, M. Biochim. Biophys. Acta 1171, 207-210, 1992
A; Title: Sequence characterization of a sheep cDNA for antithrombin III.
A; Reference number: S28219; MUID:93129622; PMID:1482684
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ó
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 431;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 82; DB 1; Length 433;
Pred. No. 2.7e-06;
1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 82; DB 1; Length 431
Pred. No. 2.7e-06;
1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      95.3%;
94.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                95.3%;
94.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 125 AKINCRLYRKANKSSEL 141
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              125 AKLNCRLYRKANKSSEL 141
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 AKLNCRLYRKANKSSKL 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 AKLNCRLYRKANKSSKL 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 95.3
Best Local Similarity 94.1
Matches 16; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          antithrombin III - bovine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Matches
                    RESULT 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   δλ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ò
```

g

```
A; Molecule type: DNA
A; Residues: 1-531 < LBO
A; Title: Molecular cloning and expression of a fifth muscarinic acetylcholine recepto
A; Title: Molecular cloning and expression of a fifth muscarinic acetylcholine recepto
A; Title: Molecular cloning and expression of a fifth muscarinic acetylcholine recepto
A; Reference number: A3354, MUID: 89214170; PMID: 2540186
A; Accession: A3354
A; Molecule type: DNA
A; Residues: 1-531 < LIIA>
A; Molecule type: DNA
A; Molecule type: Protein
A; Reference number: A37121; MUID: 90337982; PMID: 2380182
A; Accession: C37121
A; Residues: 66-128 < KUR>
A; Residues: 66-128 < KUR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         C;Species: Homo_sapiens (man)
C;Date: 31.Mar-1992 #sequence_revision 31-Mar-1992 #text_change 21-Jan-2000
C;Accession: J70530
R;Bonner, T.I.; Young, A.C.; Brann, M.R.; Buckley, N.J.
Neuron I, 403-410, 1988
A;Title: Cloning and expression of the human and rat m5 muscarinic acetylcholine rece
A;Reference number: J70530; MUID:90166521; PMID:3272174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               C.Comment: Muscarinic acetylcholine receptors mediate many of the actions of the neur C.Superfamily: vertebrate rhodopsin C.Superfamily: vertebrate rhodopsin C.Skeywords: G protein-coupled receptor; glycoprotein; neurotransmitter receptor; phos F;29-52,Domain: transmembrane #status predicted <TM2> F;66-86,Domain: transmembrane #status predicted <TM2> F;104-125,Domain: transmembrane #status predicted <TM3>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                C;Comment: Muscarinic acetylcholine receptors mediate many of the actions of the neur C;Superfamily: vertebrate rhodopsin C;Superfamily: vertebrate rhodopsin C;Keywords: G protein-roupled receptor; glycoprotein; neurotransmitter receptor; phos F;30-53/Domain: transmembrane #status predicted <TM1>
F;67-87/Domain: transmembrane #status predicted <TM2>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    muscarinic acetylcholine rece
                                                                                                                                                                                                                                                        C;Species: Rattus norvegicus (Norway rat)
C;Date: 31-Mar-1992 #sequence_revision 31-Mar-1992 #text_change 21-Jan-2000 C;Accession: JT0531, A33354; C37121
R;Bonner, T.I.; Young, A.C.; Brann, M.R.; Buckley, N.J.
Neuron 1, 403-410, 1988
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            predicted <TM6>
predicted <TM7>
(covalent) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 531;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Title: Cloning and expression of the human and rat m5 A;Reference number: JT0530; MUID:90166521; PMID:3272174 A;Accession: JT0531
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     F;146-168/Domain: transmembrane #status predicted <TM4>
F;191-213/Domain: transmembrane #status predicted <TM5>
F;443-463/Domain: transmembrane #status predicted <TM6>
F;77-49496/Domain: transmembrane #status predicted <TM6>
F;77,12/Binding site: carbohydrate (Asn) (covalent) #stat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DB 2;
36;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Pred. No. 36;
3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    muscarinic acetylcholine receptor M5 - human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 41;
                                                                                                                                                                                                                                 muscarinic acetylcholine receptor M5 - rat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      47.7%;
50.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
197 KIDCRYTREARRSAK 211
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            211 LYCRIYRETEKRTK 224
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     3 LNCRLYRKANKSSK 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A; Accession: JT0530
A; Molecule type: DNA
A; Residues: 1-532 <BON>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Best_Local Similarity
Matches 7; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            g
                                                                                                                                                                                                                                               Nithernet names: Ilpopolysaccharide N'acetylglucosaminyltransferase ytcc C; Species: Bacillus subtilis
C; Species: Speci
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Title: Complete genome sequence of Pseudomonas aeruginosa PA01, an opportunistic pathd
A;Reference number: A82950; MUID:20437337; PMID:10984043
A;Accession: D83380
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     P.; Hickey, M.J.; Br
A.; Larbig, K.; Lim,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Status: preliminary; nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-407 <KUNA
A;Crossreferences: GB:299119; GB:AL009126; NID:92635411; PIDN:CAB15066.1; PID:92635572
A;Experimental source: strain 168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ó
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  hypothetical protein PA2133 [imported] - Pseudomonas aeruginosa (strain PA01)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       C.Species: Pseudomonas aeruginosa
C.Date: 15-5ep-2000 #sequence_revision 15-Sep-2000 #text_change 31-Dec-2000
C.Accession: D8380
R.Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warrener, P.; Hick
adman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larb
Nature 406, 959-964, 2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         .;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ;
                                                                                                                                                                                                                                 probable hexosyltransferase (EC 2.4.1.-) ytcc - Bacillus subtilis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 407;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB 2; Length 285,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 C;Superfamily: probable hexosyltransferase ytxN
C;Keywords: glycosyltransferase; hexosyltransferase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 42; DB 1;
Pred. No. 19;
4; Mismatches 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Pred. No. 21;
5; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     47.7%; Score 41;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Experimental source: strain PAO1 C; Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              46.78;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LNVSLYKKASPNSKI 104
    1359 INVRLYEKYNKENK 1372
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       3 LNCRLYRKANKSSKL 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2 KLNCRLYRKANKSSK 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity
Matches 7; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A; Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Gene: PA2133
```

90

οp

ŏ

ò

ö

Gaps

```
A;Molecule type: DNA
A;Residues: 1-318 <R005
A;Cross-references: EMBL:313290; NID:946747; PIDN:CAA31648.1; PID:946749
A;Cross-references: EMBL:40.1990
R;Burdeska, A.; Ott, M.; Bannwarth, W.; Then, R.L.
FBBS Lett. 266, 159-165, 1990
A;Title: Identical genes for trimethoprim-resistant dihydrofolate reductase from Stap
A;Reference number: $10715; MUID:90306343; PMID:2365064
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               transport ATP-binding protein msbA homolog MG014 - Mycoplasma genitalium C:Specias: Mycoplasma genitalium C:Specias: Mycoplasma genitalium C:Date: 17-Nov-1995 #sequence_revision 17-Nov-1995 #text_change 02-Feb-2001 C;Accession: E64201
R:Fraser, C.M.; Gocayne, J.D.; White, O.; Adams, M.D.; Clayton, R.A.; Fleischmann, R. M.: Fuhrmann, J.; Nguyen, D.; Utterback, T.R.; Saudek, D.M.; Phillips, C.A.; Merrick, C.A.; Vencer, J.C.
Science 270, 397-403, 1995
A:Title: The minimal gene complement of Mycoplasma genitalium.
A:Feference number: A64200; MUID:96026346; PMID:7569993
A:Accession: E64201
A:Status: prealiminary; nucleic acid sequence not shown; translation not shown A:Molecule type: DNA
A:Residues: 1-623 <TIGR>
A:Residues: 1-624 <TIGR>
A:Residues: 1-625 <TIGR>
A:Re
                                                                                                                                                                                                                                      C; Species: Staphylococous aureus
C; Date: 31-Mar-1993 #sequence_revision 31-Mar-1993 #text_change 11-Jun-1999
C; Accession: S04163; $14478
R; Rouch, D.A.; Messerotti, L.J.; Loo, L.S.L.; Jackson, C.A.; Skurray, R.A.
Mol. Microbiol. 3, 161-175, 1989
A; Title: Trimethoprim resistance transposon Tn4003 from Staphylococcus aureus encodes
A; Reference number: S04162; MUID: 89343620; PMID: 2548057
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A)Genetic code: SGC3
C;Superfamily: unassigned ATP-binding cassette proteins; ATP-binding cassette homolog
C;Keywords: ATP; nucleotide binding; P-loop
F;383-587/Domain: ATP-binding cassette homology <ABC>
F;400-407/Region: nucleotide-binding motif A (P-loop)
                                                                                                                                                                                           thymidylate synthase (EC 2.1.1.45) - Staphylococcus aureus plasmid pSK1 transposon Tn
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A. Accession: S14178
A. Status: preliminary; translation not shown
A. Status: preliminary; translation not shown
A. Status: preliminary; translation not shown
A. Status: DNA
A. Molecule type: DNA
A. Cross-references: EMBL: Y07536; NID: 946551; PIDN: CAA68823.1; PID: 946552
C. Genetios:
A. Gene: thyA
A. Gene: thyA
A. Gene: plasmid
A. C. Superifamily: thymidylate synthase; thymidylate synthase homology
C. Keywords: decoxyribonucleotide biosynthesis; methyltransferase
F. G. 318/Domain: thymidylate synthase homology < TDS>
F. C. Status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DB 2; Length 623;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DB 1; Length 318;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 40; DB 1
Pred. No. 34;
4; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       46.5%; Score 40; DB
53.8%; Pred. No. 62;
tive 2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Experimental source: strain G-37 C; Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       46.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 46.5
Best Local Similarity 60.0
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Best_Local Similarity 53.8
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              4 NCRLYRKANKSSK 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1|||:||:::
213 KLNCQLYQRS 222
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2 KLNCRLYRKA 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Accession: S04163
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   δλ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      hypothetical protein T21L8.80 - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 13-Aug-1999 #sequence_revision 13-Aug-1999 #text_change 20-Jun-2000
C;Accession: T12988
R;Choisne, N.; Robert, C.; Brottier, P.; Wincker, P.; Cattolico, L.; Artiguenave, F.; Sa submitted to the Protein Sequence Database, July 1999
A;Accession: T12988
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            C; Species: Clostridium acetobutylicum C; Jobanes: Clostridium acetobutylicum C; Jobanes: L4-Sep-2001 #sequence_revision 14-Sep-2001 #text_change 30-Sep-2001 C; Jobanes: D97281 E; Jobanes: D97281 E; Jobanes: Jo
                                                                                                                                                                                                                                                                                                                                                                                                                             ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Cross-references: GB:AE001437; PIDN:AAK81039.1; PID:915026164; GSPDB:GN00168 A;Experimental source: Clostridium acetobutylicum ATCC824
                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 pseudouridylate synthase, TRUA [imported] - Clostridium acetobutylicum
                                      F;147-169/Domain: transmembrane #status predicted <TW4>
F;192-214/Domain: transmembrane #status predicted <TW5>
F;444-464/Domain: transmembrane #status predicted <TW6>
F;479-498/Domain: transmembrane #status predicted <TW6>
F;479-498/Domain: transmembrane #status predicted <TW7>
F;8,13/Binding site: carbohydrate (Asn) (covalent) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Map position: 3
A;Introns: 106/3; 374/3; 427/3; 606/1
C;Superfamily: Arabidopsis thaliana hypothetical protein F18N11.140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A; Modecule type: DNA
A; Residues: 1-664 <CHO>
A; Cross-references: EMBL:AL096860; GSPDB:GN00061; ATSP:T21L8.80
A; Experimental source: cultivar Columbia; BAC clone T21L8
C; Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 40; DB 2; Length 244; Pred. No. 27;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 664;
                                                                                                                                                                                                                                                                                                                             Score 41; DB 2; Length 532
                                                                                                                                                                                                                                                                                                                                                                                                                             4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 41; DB 2;
Pred. No. 44;
F;105-126/Domain: transmembrane #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                        3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         C; Superfamily: tRNA-pseudouridine synthase I
                                                                                                                                                                                                                                                                                                                                                                                  Pred. No.
                                                                                                                                                                                                                                                                                                                             47.78;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                47.78;
66.78;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              46.5%;
66.7%;
                                                                                                                                                                                                                                                                                                                                                                   ilarity 50.0%;
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 212 LYCRIYRETEKRIK 225
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               3 LNCRLYRKANKSSK 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               245 LNCREYPKNNKT 256
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ||||| | |:| |
| 134 KLNCDLMREATK 145
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity
8, Conserva
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             3 LNCRLYRKANKS 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2 KLNCRLYRKANK 13
                                                                                                                                                                                                                                                                                                                                                                   Best_Local Similarity
Matches 7; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity
Matches 8; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A; Molecule type: DNA
A; Residues: 1-244 <KUR>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Gene: ATSP: T21L8.80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A; Accession: D97281
A; Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       C;Genetics:
A;Gene: CAC3099
                                                                                                                                                                                                                                                                                                                             Query Match
                                                                                                                                                                                                                                                                                                                                                                                                               Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               QQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    δy
```

÷

Gaps

; 0

ö

Gaps

# 601 NCSLYQKMKESQK 613 qq

```
Cipate: 19-May-2000 #sequence_revision 19-May-2000 #text_change 08-Sep-2000 Cipate: 10-May: Kuspa, A.; Loomis, W.F. Proc. Natl. Acad. Sci. U.S.A. 91, 9446-9450, 1994 A;Title: Discovery of myosin genes by physical mapping in Dictyostelium. A;Reference number: 220873; MuID:95023928; PMID:7937787 A;Accession: A59249 A;Status is predict type: DNA A;Status is predict type: DNA A;Residues: 1-2357 CTIT> A;Cross references: GB:L35231; NID:96226760; PIDN:AAF06035.1; PID:96226761 A;Residues: 1-2357 CTIT> A;Cross references: GB:L35231; NID:96226760; PIDN:AAF06035.1; PID:96226761 A;Residues: 1-237 CTIT> A;Cross references: GB:L35231; NID:96226760; PIDN:AAF06035.1; PID:96226761 A;Reference number: A59249 A;Title: A class VII unconventional myosin is required for phagocytosis. A;Reference number: A59249 A;Contents: annotation C;Superfamily: myosin motor domain homology <a href="Monostrange">Monostrange</a> C;Superfamily: myosin motor domain homology <a href="Monostrange">Monostrange</a> C;Superfamily: myosin motor domain homology
```

; 0

Gaps

. 0

Query Match 46.5%; Score 40; DB 2; Length 2357; Best Local Similarity 37.5%; Pred. No. 2e+02; Matches 6; Conservative 6; Mismatches 4; Indels

Search completed: December 2, 2002, 10:04:53 Job time : 4.04478 secs

2 KLNCRLYRKANKSSKL 17

ò

```
GenCore version 5.1.3 Copyright (c) 1993 - 2002 Compugen Ltd.
```

OM protein - protein search, using sw model

December 2, 2002, 09:59:55; Search time 1.69154 Seconds (without alignments) 416.837 Million cell updates/sec Run on:

1 AKLNCRLYRKANKSSKL 17 US-09-741-106-12 86 Title: Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

112892 seqs, 41476328 residues Searched:

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 08
Maximum Match 1008
Listing first 45 summaries

SwissProt\_40:\* Database : Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	neines omod 80100	pos t	7.0	mus m	ratt		macac		_	034685 bacillus su	sciara c	neisse		Q03376 chironomus		O18830 ovis aries			_	marburg	Ω			Q9pir1 campylobact	P49018 saccharomyc		P24045 gallus gall			Q12704 schizosacch	-		
SUMMARIES		ANT3_HUMAN	ANT3_BOVIN	ANT3_SHEEP	ANT3_MOUSE	ACM5_RAT	ACM5_HUMAN	ACM5_MACMU	TYSY_STAAU	Y014_MYCGE	YOFA_BACSU	PO21_SCICO	LBPA_NEIMB	LBPA_NEIMA	BAR3_CHITE	BIMB_EMENI	GDF8_SHEEP	UDG_RICPR	ACH3_DROME	VGP_MABVM	VGP_MABVP	HMMR_HUMAN	G156_PARPR	RS15_METTH	PYRE_CAMJE	GPI8_YEAST	GUNB_FUSOX	GAB4_CHICK	YDSB_SCHPO	YDM6_SCHPO	DPOG_SCHPO	NXP1_MACMU	NXP1_MOUSE	NXP1_HUMAN
	Length DB	464							318 1																								~	_
о¥Р	Query	100	95.3	95.3	93.0	47.7	47.7		46.5									4	4.	4.	4.	₹.	4.	ب	'n,	43.0	m ,	m .	<u>.</u>	m,	·,	ď.	42.4	42.4
	Score	98	82	82	80	41	41	41	40	40	9.0	39	3.0	50 C	9,0	98	30 C	χ. Υ. (	30 00	88	38	80 0	9 1	٧,	3,	37	3.7	3.7	3.7	37	,	36.5	യ	o
	Result No.	П	7	m	4	Ŋ	9	7	ω (	2,6	7.	T	77	13	T T	C 1	T P	17	80 C	J (	20	770	77	223	# L	72	970	17	87	5.2	300	31	32	33

Q63366 rattus norv P57797 cricetulus O19052 oryctolagus P3724 xenopus lae O62807 sus scrofa O18971 bos taurus P3721 homo sapien O18924 macaca mula P37238 mus musculu O88275 rattus norv P31630 cowpea seve P39715 saccharomyc
NXP1_RAT PPAT_CRIGR PPAT_CRIGR PPAT_XEBLT PPAT_XEBLA PPAT_BIG PPAT_HUMAN PPAT_MACMU PPAT
наннаннана
271 475 477 477 504 505 505 505 505 1002
44444444446 444444444444
$\begin{array}{cccccccccccccccccccccccccccccccccccc$
88888888888888888888888888888888888888

## ALIGNMENTS

a

```
MEDLINE-91192143; PubMed-2013320;
Austin R.C., Rachubinski R.A., Blachjman M.A.;
"Site-directed mutagenesis of alanine-382 of human antithrombin III.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE-94373498; PubMed-8087553;
Carrell R.W., Stein P.E., Fermi G., Wardell M.R.;
Hological implications of a 3 A structure of dimeric antithrombin.";
Structure 2:257-270(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                X-RAY CRYSTALLOGRAPHY (3.2 ANGSTROMS).
MEDLINE-95384753; PubMed-7656006;
Schreuder H.A., de Boer B., Dijkema R., Mulders J., Theunissen H.J.M.,
Grootenhuis P.D.J., Hol W.G.J.,
"The intact and cleaved human antithrombin III complex as a model for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDINE-94054339; PubMed-8236149;
Lane D.A., Olds R.J., Boisclair M., Chowdhury V., Thein S.L.,
Cooper D.N., Blajchman M., Perry D., Emmerich J., Alach M.;
"Antithrombin III mutation database: first update. For the Thrombin
and its Inhibitors Subcommittee of the Scientific and Standardization
Committee of the International Society on Thrombosis and
Haemostasis.";
                                                                                                                                                    MEDLINE-81212814; PubMed-7238875;
Bjoerk I., Danielsson A., Fenton J.W. II, Joernvall H.;
"The site in human antithrombin for functional proteolytic cleavage
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Skinner R., Abrahams J.-P., Whisstock J.C., Lesk A.M., Carrel R.W., Wardell M.R.;
                                                                                                                                                                                                                                                                                       MEDLINE-84111578; Pubmed-6693405; Blackburn M.N., Smith R.L., Carson J., Sibley C.C.; The heparin-binding site of antithrombin III. Identification of a critical tryptophan in the amino acid sequence."; Biol. Chem. 259:939-941(1984).
            "Primary structure of antithrombin-III (heparin cofactor). Partial homology between alpha-1-antitrypsin and antithrombin-III."; (In) Collen D., Wiman B., Verstraete M. (eds.); The physiological inhibitors of blood coagulation and fibrinolysis,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "The 2.6 A structure of antithrombin indicates a conformational change at the heparin binding site."; J. Mol. Biol. 266:601-609(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDILINE-88437366; PubMed-9761669; Skinner R., Chang W.S.W., Jin L., Pei X.Y., Huntington J.A., Abrahams J.-P., Carrell R.W., Lomas D.A.; Implications for function and therapy of a 2.9 A structure of binary-complexed antithrombin."; J. Mol. Biol. 283:9-14(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDIINE=91129302; PubMed=2126464;
MOUTCY L., Samama J.-P., Delarue M., Choay J., Lormeau J.C.,
Petittou M., Moras D.;
"Antithrombin III: structural and functional aspects.";
Biochimie 72:599-608(1990).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     K-RAY CRYSTALLOGRAPHY (3.0 ANGSTROMS).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           X-RAY CRYSTALLOGRAPHY (2.6 ANGSTROMS).
MEDLINE-97220238; Pubmed=9067613;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      X-RAY CRYSTALLOGRAPHY (2.9 ANGSTROMS).
                                                                                               pp.43-54, Elsevier, Amsterdam (1979).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               serpin-proteinase interactions."
Nat. Struct. Biol. 1:48-54(1994)
                                                                                                                                                                                                                                   FEBS Lett. 126:257-260(1981).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FEBS Lett. 280:254-258(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                   MUTAGENESIS OF ALA-414.
                                                                                                                                                                                                                                                                            HEPARIN-BINDING SITE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      REVIEW ON VARIANTS.
                                                                                                                                                                                                                  human thrombin.
Magnusson S.;
                                                                                                                                      ACTIVE SITE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  REVIEW
```

```
Borg J.Y., Brennan S.O., Carrell R.W., George P., Perry D.J., Shaw J.; "Antithrombin Rouen IV 24 Arg-->Cys. The amino-terminal contribution to heparin binding.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Erdjument H., Laned D.A., Panico M., di Marzo V., Morris H.R.; "Single amino acid substitutions in the reactive site of antithrombin leading to thrombosis. Congenital substitution of arginine 393 to cysteine in antithrombin Northwick Park and to histidine in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Devzak-Kizuk R., Chui D.H.K., Prochownik E.V., Carter C.J., Ofosu F.A., Blajchman M.A.;
"Antithrombin-III-Hamilton: a gene with a point mutation (quanine to adenine) in codon 382 causing impaired scrine protease reactivity."; Blood 72:1518-1523(1988).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Chang J.Y., Tran T.H., "Antithrombin III Basel. Identification of a Pro-Leu substitution in a hereditary abnormal antithrombin with impaired heparin cofactor
                                                                                                                                                                                                                                                                            Bock S.C., Marrinan J.A., Radziejewska E.; "Antithrombin III Utah: proline-407 to leucine mutation in a highly conserved region near the inhibitor reactive site."; Biochemistry 27:6171-6178(1988).
                                                                                                                                                                                                                                                                                                                                                                                                  Koide T., Odani S., Takahashi K., Ono T., Sakuragawa N.; "Antithrombin III Toyama: replacement of arginine-47 by cysteine in hereditary abnormal antithrombin III that lacks heparin-binding
                           MEDLINE-95269065; PubMed=7749926;
Stein P.E., Carrell R.W.;
"What do dysfunctional serpins tell us about molecular mobility and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Antithrombin Chicago, amino acid substitution of arginine 393 to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Erdjument H., Lane D.A., Panico M., di Marzo V., Morris H.R.,
Bauer K., Rosenberg R.D.;
                                                                                                                                                   MEDLINE-96263733; PubMed-8664906;
Perry D.J., Carrell R.W.;
"Molecular genetics of human antithrombin deficiency.";
Hum. Mutat. 7:7-22(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Stephens A.W., Thalley B.S., Hirs C.H.W.;
"Antithrombin-III Denver, a reactive site variant.";
J. Biol. Chem. 262:1044-1048(1987).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Proc. Natl. Acad. Sci. U.S.A. 81:289-293(1984).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     VARIANTS GLASCOW AND NORTHWICK-PARK.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            antithrombin Glasgow.";
J. Biol. Chem. 263:5589-5593(1988).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    activity.";
J. Biol. Chem. 261:1174-1176(1986).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE=87109210; PubMed=3805013;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE=88186869; PubMed=3162733;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE=90306344; PubMed=2365065;
                                                                                                     Struct. Biol. 2:96-113(1995)
                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE=84119472; PubMed=6582486;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              VARIANT CHICAGO.
MEDLINE=89388698; PubMed=2781509;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE-86111754; PubMed-3080419;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE-89027076; PubMed=3179438;
                                                                                                                                                                                                                                                              MEDLINE=89050967; PubMed=3191114;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Thromb. Res. 54:613-619(1989).
                REVIEW ON VARIANTS.
                                                                                                                                          REVIEW ON VARIANTS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             VARIANT HAMILTON.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        VARIANT ROUEN-4.
                                                                                                                                                                                                                                                                                                                                                                       VARIANT TOYAMA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       VARIANT DENVER.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               VARIANT BASEL.
                                                                                                                                                                                                                                                 UTAH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    histidine."
                                                                                    disease?";
                                                                                                                                                                                                                                                 VARIANT
                                                                                                                                                                                                                                                                                                                                                                                                                                                               ability
```

```
RESULT 3
                                   qq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ò
                        ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
                                                                                                                                                                                                                                                                                     Mejdoub H., le Ret M., Boulanger Y., Maman M., Choay J., Reinbolt J.; "The complete amino acid sequence of bovine antithrombin (ATIII).", J. Protein Chem. 10:205-212(1991).
                        Gaps
                                                                                                                                                                                                                                                                                                                                           MEDLINE-93323115; PubMed-8331659;
Mourey L., Samama J.-P., Delarue M., Petitou M., Choay J., Moras D.;
"Crystal structure of cleaved bovine antithrombin III at 3.2-A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                 Bos taurus (Bovine).
Sukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
Bovidae; Bovinae; Bos.
                                                                                                                                                                                                                                                                                                                                                                                   J. Mol. Biol. 232:223-241(1993).

-! FUNCTION: MOST IMPORTANT SERIDE PROTEASE INHIBITOR IN PLASMA THAT REGULATES THE BLOOD COAGULATION CASCADE. AT ILI INHIBITS THE MEDIA AS FACTORS IXA, XA AND XIA. ITS INHIBITORY ACTIVITY IS GREATLY ENHANCED IN THE PRESENCE OF HEPARIN.
-!- SUBCELLULAR LOCATION: Extracellular.
-!- SIMLEARIY: PLASMA.
-!- SIMLEARIY: SIACU-94.
-!- SIMLEARIY: SIACU-94.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PROSITE; PS00284; SERPIN; 1.
Serpin; Serine protease inhibitor; Glycoprotein; Heparin-binding;
Plasma; Blood coagulation; 3D-structure.
                        ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0;
100.0%; Score 86; DB 1; Length 464; 100.0%; Pred. No. 2e-07; Live 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 82; DB 1; Length 433;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              N-LINKED (GLCNAC. . .).
F6295B3F0195E9A9 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     cogulation; 3D-structure.
50 50 HEPARIN (BY SIMILARITY).
30 130 HEPARIN (BY SIMILARITY).
46 HEPARIN (BY SIMILARITY).
94 395 REACTIVE BOND.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (GLCNAC. . .).
(GLCNAC. . .).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             N-LINKED (GLCNAC. . .).
N-LINKED (GLCNAC. . .).
N-LINKED (GLCNAC. . .).
                                                                                                                                                       Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1; Mismatches
                                                                                                                                                                                                                                                                                                                                  X-RAY CRYSTALLOGRAPHY (3.2 ANGSTROMS).
                                                                                                                                                                                                                                                                           MEDLINE=92029517; Pubmed=1930634;
                                                                                                                                         01-NOV-1995 (Rel. 32, Created)
01-NOV-1995 (Rel. 32, Last seq
16-OCT-2001 (Rel. 40, Last anno
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         49126 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               95.3%;
                                                      156 AKLNCRLYRKANKSSKL 172
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Pfam; PF00079; serpin; 1.
SMART; SM00093; SERPIN; 1.
                                                                                                                                                                           Antithrombin-III (ATIII).
                                          1 AKLNCRLYRKANKSSKL 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 AKLNCRLYRKANKSSKL 17
                     17; Conservative
                                                                                                                       STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        433 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Best Local Similarity
                                                                                                                                                                                                                                          NCBI_TaxID-9913;
                                                                                                                                                                                     SERPINC1 OR AT3.
                                                                                                                                                                                                                                                                                                                                                                               resolution.";
                                                                                                                     ANT3_BOVIN
P41361;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     BINDING
ACT_SITE
DISULFID
DISULFID
                                                                                                                                                                                                                                                                SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                BINDING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              BINDING
                                                                                                            ANT3_BOVIN
                     Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Matches
                                                                                                 RESULT 2
                                                               q
                                                                                                                       ά
```

g

```
This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation-the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                           Ovis aries (Sheep).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
N-LINKED (GLCNAC. ..) (POTENTIAL).
N-LINKED (GLCNAC. ..) (POTENTIAL).
N-LINKED (GLCNAC. ..) (POTENTIAL).
N-LINKED (GLCNAC. ..) (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Interro; issues in 1.
SMARY; SW00093; SERPIN; 1.
PROSITE; PS00284; SERPIN; 1.
Serpin; Serine protease inhibitor; Glycoprotein; Heparin-binding; Plasma; Blood coaqulation; Signal.
Plasma; Blood coaqulation; Signal.
By SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 82; DB 1; Length 465;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               52499 MW; E075EFAE51D5F118 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           HEPARIN (BY SIMILARITY).
HEPARIN (BY SIMILARITY).
HEPARIN (BY SIMILARITY).
REACTIVE BOND.
                                             01-0CT-1993 (Rel. 27, Created)
01-0CT-1993 (Rel. 27, Last sequence update)
16-0CT-2001 (Rel. 40, Last annotation update)
Antithrombin-III precursor (ATIII).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Pred. No. 1e-06;
1; Mismatches
                 465 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      465 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL, X68287; CAA48347.1; -. PIR; S28219, S28219. HSSP; P01008; IATH. InterPro; IPR000215; Serpin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                95.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 AKLNCRLYRKANKSSKL 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Local Similarity 94.1
Les 16; Conservative
                 STANDARD;
                                                                                                                                                                                Bovidae; Caprinae; Ovis.
NCBI_TaxID=9940;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          465
1162
1178
1178
1128
1129
1129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            41
54
280
129
168
188
225
465 AA;
                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
                                                                                                                   SERPINC1 OR AT3.
             ANT3_SHEEP
P32262;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ANT3_MOUSE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ACT_SITE
DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         BINDING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            BINDING
ANT3_SHEEP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ANT3_MOUSE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Best
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   П
```

```
Muscarinic acetylcholine receptor M5
            CHRM5 OR CHRM-5
                                                                                                                                                                          Birnbaumer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MOD_RES
MOD_RES
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TRANSMEM
DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Matches
   between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEALLINE
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
N-LINKED (GLCNAC. .) (POTENTIAL).
N-LINKED (GLCNAC. .) (POTENTIAL).
N-LINKED (GLCNAC. .) (POTENTIAL).
                                                                                                                                                                    Thromb. Haemost. 68:291-296(1992).

-i- FUNCTION: MOST IMPORTANT SERINE PROTEASE INHIBITOR IN PLASMA
THAT REGULARES THE BLOOD COAGULATION CASCADE. AT-III INHIBITS
THAT REGULARES THE BLOOD COAGULATION CASCADE. AT-III INHIBITS
THROMBIN AS WELL AS FACTORS IXA, XA AND XIA. ITS INHIBITORY
ACTIVITY IS GREATLY ENHANCED IN THE PRESENCE OF HEPARIN.
-i- SUBCELLULAR LOCATION: EXTRACHILLIAR.
-i- TISSUE SPECIFICITY: PLASMA.
-i- SIMILARITY: BELONGS TO THE SERPIN FAMILY.
                                                                                                                                                                                                                                                                                                                                                                MGD; MGI:88095; Serpinc1.
InterPro: IPR00215; Serpin.
Pfam; PF00079; Serpin. 1.
SMART: SMO0093; SERPIN: 1.
PROSITE; PS00284; SERPIN; 1.
Serpin; Serine protease inhibitor; Glycoprotein; Heparin-binding;
                                                                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Musinae; Mus
                                                                                                                                        Wu J.K., Sheffield W.P., Blajchman M.A.; "Molecular cloning and cell-free expression of mouse antithrombin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              .
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DB 1; Length 465;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 80; DB 1; Lung-
Pred. No. 2.2e-06;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SCE087E98874E35D CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                             ANTITHROMBIN-III.
HEPARIN (BY SIMILARITY).
HEPARIN (BY SIMILARITY).
HEPARIN (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Last sequence update)
Last annotation update)
                 (Rel. 27, Created)
(Rel. 27, Last sequence update)
(Rel. 40, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        531 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                     BY SIMILARITY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        REACTIVE BOND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRT;
                                             Antithrombin-III precursor (ATIII).
                                                                                                                                                                                                                                                                                                                                                                                                                             coagulation; Signal
                                                                                                                               MEDLINE=93069082; PubMed=1440494;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (Rel. 09, Created)
(Rel. 09, Last sequ
(Rel. 32, Last anno
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        52003 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            93.08;
94.18;
                                                                                                                                                                                                                                                                                                                                             EMBL; S47225; AAB23965.1; *. HSSP; P01008; 1ATH.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              157 AKLNCRLYRKANKSSDL 173
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 AKLNCRLYRKANKSSKL 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Local Similarity 94.1 les 16; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                               465
82
162
178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        427
1161
1128
463
1129
1168
1188
                                                                      Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AA;
                                                                                                                       SEQUENCE FROM N.A.
                  01-OCT-1993 (Rel.
                                                                                                 NCBI_TaxID=10090;
                                                          SERPINC1 OR AT3
                                                                                                                                                                                                                                                                                                                                                                                                                              Plasma; Blood
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-NOV-1988 (
01-NOV-1988 (
01-NOV-1995 (
                            01-OCT-1993
16-OCT-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ACM5_RAT
P08911;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ACT_SITE
DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                           BINDING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                BINDING
                                                                                                                                                                                                                                                                                                                                                                                                                                         SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                    CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ACM5_RAT
         g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DT DT
```

```
This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is no no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                    receptor ";
J. Biol. Chem. 264:7328-7337(1989).
J. Biol. Chem. 264:7328-7337(1989).
-!- FUNCTION: THE MUSCARINIC ACETYLCHOLINE RECEPTOR MEDIATES VARIOUS
-!- FUNCTION: THE PROSPOSES, INCLUDING INHIBITION OF ADDRIATATE CYCLASE,
BREAKDOWN OF PHOSPHOINOSITIDES & MODULATION OF POTASSIUM CHANNELS
THROUGH THE ACTION OF G PROTEINS. PRIMARY TRANSDUCING EFFECT IS PI
                                                                                                                                                                                                                                                                                                                              Birnbaumer L.; "Molecular cloning and expression of a fifth muscarinic acetylcholine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
Rattus norvegicus (Rat).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -i- SUBCELLULAR LOCATION: Integral membrane protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CYTOPLASMIC (POTENTIAL).
N-LINKED (GLCNAC. . .) (POTENTIAL).
                                                                                                                                                                                                                                                                                        Liao C.-F., Themmen A.P.N., Joho R., Barberis C., Birnbaumer M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 531;
                                                                                                        SEGUENCE FROM N.A.
BDDLINE-2016521; PubMed-3272174;
BODNET T.I., Young A.C., Brann M.R., Buckley N.J.;
"Cloning and expression of the human and rat m5 muscarinic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PHOSPHORYLATION (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        6 (POTENTIAL).
EXTRACELLULAR (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 (POTENTIAL).
CYTOPLASMIC (POTENTIAL).
2 (POTENTIAL).
EXTRACELLULAR (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           3 (POTENTIAL).
CYTOPLASMIC (POTENTIAL).
4 (POTENTIAL).
EXTRACELLULAR (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PHOSPHORYLATION (POTENTIAL 647CE0D5D75A2BB1 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              5 (POTENTIAL).
CYTOPLASMIC (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   47.7%; Score 41; DB 1;
50.0%; Pred. No. 13;
Live 3; Mismatches 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  7 (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SIMILARITY
                                                                                                                                                                                                                                                       SEQUENCE FROM N.A. MEDLINE=89214170; Pubmed=2540186;
                                                                                                                                                                                        acetylcholine receptor genes.";
Neuron 1:403-410(1988).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 60136 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL; M22926; AAA41672.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    442
463
477
497
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       28,
52,
65,
86,
103,
125,
145,
190,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 531 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Best Local Similarity
                                                                  NCBI_TaxID=10116;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             29
53
66
87
104
126
```

```
This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation-the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                         -1- SUBCELLUAR LOCATION: Integral membrane protein.
-1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MIN, 1104970

DIACEPPO, 108000276; GFCR_Rhodpsn.

PERMITS; PR00037; GPCRRHODOPSN.

PROSITE; PS00237; G_PROTEIN_RECEP_FI_1; 1.

PROSITE; PS50262; G_PROTEIN_RECEP_FI_2; 1.

POSISYED; PS50262; G_PROTEIN_RECEP_FI_2; 1.

Postsynaptic membrane; Ionic channel; Glycoprotein; Transmembrane;

Phosphorylation; Multigene family; G-protein coupled receptor.

DOMAIN 1. 29 EXTRACELLULAR (POTENTIAL).
                                                                                                                                                                                                             Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia; Eutheria; Primates; Catarrhini, Hominidae; Homo.
                                                                                                                                                                                                                                                                                                     Bonner T.I., Young A.C., Brann M.R., Buckley N.J.;
Cloning and expression of the human and rat m5 muscarinic
acetylcholine receptor genes.";
Neuron 1:403-410(1988).
                                                                                                                                                                                                                                                                                                                                                                                                     Rae J.L., Shepard A.R.;
Submitted (SEP-1997) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CYTOPLASMIC (POTENTIAL).
2 (POTENTIAL).
EXTRACELLULAR (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  3 (POTENTIAL).
CYTOPLASMIC (POTENTIAL).
4 (POTENTIAL).
                                                                                                                         01-NOV-1988 (Rel. 09, Created)
01-JUN-1994 (Rel. 29, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
                                                                                                                                                      15-JUN-2002 (Rel. 41, Last annotatior
Muscarinic acetylcholine receptor M5
                                                                                                   PRT;
                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
MEDLINE=90166521; Pubmed=3272174;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL; AF026263; AAB95158.1; -. EMBL; AF385591; AAK68116.1; -. PIR; JT0530, JT0530. Genew; HGNC:1954; CHRM5. MIM; 118496; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL; M80333; AAA51569.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE OF 1-526 FROM N.A.
                                                                                                   STANDARD;
                | ||:||: | :|
211 LYCRIYRETEKRTK 224
                                                                                                                                                                                                                                                                                                                                                                                       TISSUE-Lens epithelium;
3 LNCRLYRKANKSSK 16
                                                                                                                                                                                                    Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
                                                                                                                                                                                                                                             NCBI_TaxID=9606;
                                                                                                               P08912; Q96RG7;
01-NOV-1988 (Re
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       30
54
67
88
105
127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TURNOVER.
                                                                                                 ACM5_HUMAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DOMAIN
                                                                                                                                                                                    CHRM5
                                                                                  ACM5_HUMAN
à
                           qq
```

```
ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation-the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.

TISSUE-Lens epithelium;

TISSUE-Lens epithelium;

Rae J.L., Shepard A.R.;

Submitted (SEP-1997) to the EMBL/GenBank/DDBJ databases.

-!- FUNCTION: THE MUSCARINIC ACETYLCHOLINE RECEPTOR MEDIATES VARIOUS

-!- FUNCTION: THE MUSCARINIC ACETYLCHOLINE RECEPTOR MEDIATES VARIOUS

CELLULAR RESPONSES, INCLUDING INHIBITION OF ADENYLATE CYCLASE,

BREAKDOWN OF PHOSPHOINOSITIDES & MODULATION OF POTASSIUM CHANNELS

THROUGH THE ACTION OF G PROFEINS. PRIMARY TRANSDUCING EFFECT IS PI
                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -:- SUBCELLULAR LOCATION: Integral membrane protein.
-:- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PROSITE; PS00237, G_RROTEIN_RECEP_F1_1; 1.
PROSITE; PS50262; G_RROTEIN_RECEP_F1_2; 1.
PROSITE; PS50262; G_RROTEIN_RECEP_F1_2; 1.
PROSIDIO Rembrane; Ionic channel; Glycoprotein; Transmembrane; Phosphorylation; Multigene family; G-protein coupled receptor.
DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae;
                                                                         7 (POTENTIAL).
CYTOPLASMIC (POTENTIAL).
N-LINKED (GLCNAC. . ) (POTENTIAL).
                                                                                                                                                                                                                                                ö
                                                                                                                                                                                                              Score 41; DB 1; Length 532;
Pred. No. 13;
3; Mismatches 4; Indels
                                                                                                                     BY SIMILARITY.
PHOSPHORYLATION (POTENTIAL).
PHOSPHORYLATION (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 (POTENTIAL).
CYTOPLASMIC (POTENTIAL).
2 (POTENTIAL).
EXTRACELLULAR (POTENTIAL).
3 (POTENTIAL).
                                            6 (POTENTIAL).
EXTRACELLULAR (POTENTIAL).
   EXTRACELLULAR (POTENTIAL).
                                                                                                                                                                   Q -> P (IN REF. 3).
EE846186F645DD9B CRC64;
              5 (POTENTIAL).
CYTOPLASMIC (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CYTOPLASMIC (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                            [5-JUL-1998 (Rel. 36, Created)
15-JUL-1998 (Rel. 36, Last sequence update)
15-JUL-1998 (Rel. 36, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Muscarinic acetylcholine receptor M5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL; AF026264; AAB95159.1; -.
InterPro; PR000276; GPCR_Rhodpsn.
Pfan; PF00001; 7tm.1; 1.
PRINTS; PR00237; GPCRRHODOPSN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Macaca mulatta (Rhesus macaque).
                                                                                                                                                                                  60073 MW;
                                                                                                                                                                                                              47.78;
                                                                                                                                                                                                                                             7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                    STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Cercopithecinae; Macaca.
                                                                                                                                                                                                                                                                                           | ||:||: | :|
212 LYCRIYRETEKRTK 225
                                                                                                                                                                                                                                                                           3 LNCRLYRKANKSSK 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       29,
53
66
87
104
126
                                                                                                                                                                                532 AA;
                                                                                                                                                                                                                           Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NCBI_TaxID=9544;
170
192
215
215
444
444
479
479
479
479
103
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TURNOVER.
                                                                                                                                                                                                                                                                                                                                                                                 ACM5 MACMU
                                                         DOMAIN
TRANSMEM
                                                                                                                     DISULFID
MOD_RES
MOD_RES
CONFLICT
DOMAIN
TRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TRANSMEM
DOMAIN
                                            TRANSMEM
                                                                                                        CARBOHYD
                                                                                                                                                                                SEQUENCE
                                                                                                                                                                                                              Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                  P56490;
                            DOMAIN
                                                                                         DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DOMAIN
                                                                                                                                                                                                                                                                                                                                                                  ACM5_MACMU
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CHRM5
                                                                                                                                                                                                                                             Matches
                                                                                                                                                                                                                                                                                                                                                       RESULT 7
                                                                                                                                                                                                                                Best
                                                                                                                                                                                                                                                                                                        ga
```

```
This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (see http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                           ;;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Rouch D.A., Messeroti L.J., Loo L.S.L., Jackson C.A., Skurray R.A.; "Trimethoprim resistance transposon Th4003 from Staphylococcus aureus encodes genes for a dihydrofolate reductase and thymidylate synthetase flanked by three copies of IS257."; Mol. Microbiol. 3:161-175(1989).
                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Burdeska A., Ott M., Bannwarth W., Then R.L.;
"Identical genes for trimethoprim-resistant dihydrofolate reductase from Staphylococcus aureus in Australia and central Europe.";
FEBS Lett. 266.159-162(190).
-1- CATALXTIC ACTIVITY: 5,10-methylenetetrahydrofolate + dUMP =
                                                                                                          CYTOPLASMIC (POTENTIAL).
N-LINKED (GLCNAC. . .) (POTENTIAL).
                                                                                                                                                                                                                                                           ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   --- PATHWAY: Deoxyribonucleotide biosynthesis.
--- SUBUNIT: HOMODIMER.
--- SUBUBLUIAR LOCATION: CYCOPLESMIC (By Similarity).
--- SUBUBLUIAR: BELONGS TO THE THYMIDYLATE SYNTHASE FAMILY.
                                                                                                                                                                                                                        Score 41; DB 1; Length 532;
Pred. No. 13;
3; Mismatches 4; Indels
                                                                                                                                                           PHOSPHORYLATION (POTENTIAL).
PHOSPHORYLATION (POTENTIAL).
33BCF6D67E600D79 CRC64;
4 (POTENTIAL).
EXTRACELLULAR (POTENTIAL).
                                                                              EXTRACELLULAR (POTENTIAL)
                                              (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Bacteria; Firmicutes; Bacillales; Staphylococcus
                                                                                                                                                                                                                                                                                                                                                                                                                                    01.JAN-1990 (Rel. 13, Created)
01.JAN-1990 (Rel. 13, Last sequence update)
15.JUN-2002 (Rel. 41, Last annotation update)
Thymidylate synthase (EC 2.1.1.45) (TS) (TSase).
                                 5 (POTENTIAL).
                                                                                                7 (POTENTIAL).
                                                                                                                                             BY SIMILARITY
                                                                 6 (POTENTIAL)
                                              CYTOPLASMIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       InterPro: IPR000398; Thymidylat_synt.
                                                                                                                                                                                                                                                                                                                                                                                                       PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STRAIN=157/4696;
MEDLINE=90306343; PubMed=2365064;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TRANSPOSON-Tn4003;
MEDLINE-89343620; PubMed=2548057;
                                                                                                                                                                                            60140 MW;
                                                                                                                                                                                                                          47.7%;
50.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL; X13290; CAA31648.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL; Y07536; CAA68823.1; -. PIR; S04163; YXSAT3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        dihydrofolate + dTMP.
                                                                                                                                                                                                                                      Best Local Similarity 50.0 Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                       STANDARD;
                                                                                                                                                                                                                                                                                                                       212 LYCRIYRETEKRTK 225
                                                                                                                                                                                                                                                                                         3 LNCRLYRKANKSSK 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Staphylococcus aureus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               HSSP; P00469; 4TMS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
                                                                                                                                                                                          532 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEOUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NCBI_TaxID=1280;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Plasmid pSK1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   THYA OR THYE.
                                                                                                                                                                                                                                                                                                                                                                                                      TYSY_STAAU
P13954;
                                                                                                                                                            MOD_RES
MOD_RES
SEQUENCE
                                                                                                                                                                                                                            Query Match
                                 LRANSMEM
                                                               TRANSMEM
                                                                                                TRANSMEM
                                                                                                                              CARBOHYD
                                                                                                                                               DISULFID
                                                                                                                 DOMAIN
                                                   DOMAIN
                                                                                 DOMAIN
                  DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                          TYSY_STAAU
                                                                                                                                                                                                                                                                                                                                                                        RESULT 8
                                                                                                                                                                                                                                                                                           δ
                                                                                                                                                                                                                                                                                                                         a
```

```
This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                           ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Fraser C.M., Gocayne J.D., White O., Adams M.D., Clayton R.A., Fleischmann R.D., Bult C.J., Kerlavage A.R., Sutton G., Kelley J.M., Fritchman J.L., Weidman J.F., Small K.V., Sandusky M., Fuhrmann J.L., Tomb J.-F., Dougherty B.A., Bott K.F., Hu P.-C., Lucier T.S., Peterson S.M., Snith H.O., Hutchison C.A. III, Venter J.C., The minimal gene complement of Mycoplasma genitalium.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                sequencing.";
J. Bacteriol. 175:7918-7930(1993).
-!- SUBCELLULAR LOCATION: Integral membrane protein (Potential).
-!- SIMILARITY: BELONGS TO THE ABC TRANSPORTER FAMILY. MSBA SUBFAMILY.
                                                                                                                                                                           Gaps
       Prodom; PD001180; Thymidylat_synt; 2. PROSITE; PS00091; THYMIDYLATE_SYNTHASE; 1. Transferase; Methyltransferase; Nucleotide biosynthesis; Plasmid. ACT_SITE 201 201 BY SIMILARITY. SEQUENCE 318 AA; 37178 MW: ACFABRATY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Bacteria; Firmicutes; Mollicutes; Mycoplasmataceae; Mycoplasma.
NCBI_TaxID=2097;
                                                                                                                                                                           ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STRAIN=ATCC 33530 / G-37;
MEDLINE=94075230, PubMed=8253680;
Peterson S.N., Hu P.-C., Bott K.F., Hutchison C.A. III;
"A survey of the Mycoplasma genitalium genome by using random
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SMART; SM00382; AAA; 1.
PROSITE; PS00211; ABC_TRANSPORTER; 1.
Hypothetical protein; ATP-binding; Transport; Transmembrane;
                                                                                                                                          DB 1; Length 318;
                                                                                                                                                                           0; Indels
                                                                                                                                                                                                                                                                                                                                                   P47265: 049343;
01-FEB-1996 (Rel. 33, Created)
01-FEB-1996 (Rel. 33, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Hypothetical ABC transporter ATP-binding protein MG014.
                                                                                                                                          46.5%; Score 40; DB
60.0%; Pred. No. 12;
iive 4; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Interpro; IPR003593; AAA_ATPase.
Interpro; IPR003439; ABC_transportr.
Interpro; IPR001140; ABCtranprtrTM.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pfan; PF00005; ABC_tran; 1.
Pfan; PF00664; ABC_membrane; 1.
ProDom; PD000006; ABC_transportr; 1.
Pfam; PF00303; thymidylat_synt; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ŠEČUENCE FROM N.A.
STRAIN-ATCC 33530 / G-37;
MEDLINE-96026346; PubMed-7569993;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE OF 227-333 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL; U39680; AAC71230.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL; U02235; AAA03387.1; -. TIGR; MG014; -.
                                                                                                                                                                             6; Conservative
                                                                                                                                                                                                                                                                                                                                           STANDARD;
                                                                                                                                                                                                                                       1|||:||:::
213 KLNCQLYQRS 222
                                                                                                                                                              Best Local Similarity
                                                                                                                                                                                                                2 KLNCRLYRKA 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Complete proteome.
                                                                                                                                                                                                                                                                                                                                           7014_MYCGE
                                                                                                                                             Query Match
                                                                                                                                                                                                                                                                                                          RESULT 9
Y014_MYCGE
                                                                                                                                                                               Matches
                                                                                                                                                                                                                                                                                                                                                              δ
 DR
DR
DR
SQ
SQ
```

```
A Kunst F. Ogasawara N., Moszer I., Albertini A.M., Alloni G.,

RA Azevedo V. Bertero M.G., Bessieres P., Bolotin A., Borchert S.,

Borriss R., Bourster L., V., Eans A., Braun M., Briggell S.C., Bron S.,

RA Brouillet S., Bruschi C.V., Caldwell B., Capuano V., Carter N.M.,

Choi S.K., Codani J.J., Connerton I.F., Cummings N.J., Daniel R.A.,

Broin S.K., Codani J.J., Connerton I.F., Cummings N.J., Daniel R.A.,

RA Denizot F., Devine K.M., Dusterhoft A., Errichich S.D., Emmerson P.T.,

RA Entian K.D., Errington J., Fabret C., Ferrari E., Foulger D.,

RA Ghim S.Y., Glaser P., Goffeau A., Golightly E.J., Grandi G.,

RA Ghim S.Y., Glaser P., Goffeau A., Golightly E.J., Handt A.,

RA Hilbert H., Holsappel S., Hosono S., Hullo M.F., Itaya M., Jones L.,

RA Joris B., Karamata D., Kasahara Y., Klaerr Blanchard M., Klein C.,

RA Kobayashi Y., Koetter P., Koningstein G., Krogh S., Kumano M.,

RA Lee S.M., Levine A., Liu H., Masuda S., Maudel C., Medigue C.,

RA Dorno D., O'Reilly M., Ogawa K., Ogiwara A., Oudega B., Park S.H.,

RA Parro V., Pohl T.M., Portetelle D., Porwollik S., Rey M., Reynolds S.,

RA Rager M., Rivolta C., Rocha E., Roche B., Rose M., Sadaie Y.,

RA Sato T., Scanlan E., Schloeter R., Scoffone F.,

RA Takeuchi M., Tacconi E., Takapashi H., Takemaru K.,

RA Takeuchi M., Tacconi E., Takapashi H., Takemaru K.,

RA Takeuchi M., Tacconi E., Takapashi H., Takemaru K.,

RA Takai A., Wambutt R., Wedler E., Wedler F., Vassarotti A.,

Varia A., Wambutt R., Wedler E., Wedler H., Weitzenegger T.,

Winters P., Wipat A., Yamamoto H., Yaname K., Yasumoto K., Yata K.,

RA Tosato V., Uchiyama S., Vandenbol M., Vannater F., Vassarotti A.,

Wanters P., Wipat A., Yamamoto H., Yaname K., Yasumoto K., Yata K.,

RA The complete genome sequence of the Gram-positive bacterium Bacillus

RA The Chill R., The Complete Genome sequence of the Gram-positive bacterium Bacillus
                                                                                                                                                                                                                                            ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way
                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                          ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Nature 390:249-256(1997).
-!- SIMILARITY: BELONGS TO THE LYSR FAMILY OF TRANSCRIPTIONAL
                                                                                                                                                                                                 DB 1; Length 623;
                                                                                                                                                                                                                                          4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
NCBL_raxID=1423;
                                                                                              POTENTIAL,
ATP (POTENTIAL).
FNR -> LIV (IN REF. 2).
F5D46215C9A95DDB CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                   30-MAY-2000 (Rel. 39, Created)
30-MAY-2000 (Rel. 39, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Hypothetical transcriptional regulator yofA.
                                                                                                                                                                                                                                      2; Mismatches
                                                                                                                                                                                                                       Pred. No. 23;
                                         POTENTIAL. POTENTIAL.
                                                                                POTENTIAL.
                                                                                                                                                                                                 Score 40;
    POTENTIAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE=98044033; PubMed=9384377;
                                                                                                                                                          69536 MW;
                                                                                                                                                                                                 46.5%;
                                                                                                                                                                                                                   53.8%;
                                                                                                                                                                                                                                        7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                    STANDARD;
                                                                                                                                                                                                                                                                                                   || ||:| :| |
601 NCSLYQKMKESQK 613
                                                                                                                                                                                                                                                                             4 NCRLYRKANKSSK 16
                                                                                                                                                        623 AA;
                                                                                                                                                                                                                   Best Local Similarity
Matches 7; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Bacillus subtilis.
  27
81
157
181
266
307
331
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  REGULATORS.
                                                                                                                                                                                                                                                                                                                                                                                                              YOFA_BACSU
034685;
TRANSMEM
TRANSMEM
TRANSMEM
                                                                                                                   NP_BIND
CONFLICT
                                                                                                                                                          SEQUENCE
                                                                                                                                                                                               Query Match
                                                         TRANSMEM
                                                                         TRANSMEM
                                                                                                TRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                              YOFA_BACSU
                                                                                                                                                                                                                                                                                                                                                                           RESULT 10
                                                                                                                                                                                                                                                                                                                  Ω
ŏ
```

```
and for commercial
                    (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE=93196484; PubMed=8383793;
Burke W.D., Eickbush D.G., Xiong Y., Jakubczak J.L., Eickbush T.H.;
Burke W.D., Eickbush D.G., Xiong Y., Jakubczak J.L., Eickbush T.H.;
Sequence relationship of retrotransposable elements R1 and R2 within and between divergent insect species.";
Mol. Biol. Evol. 10:163-185(1993).
-!- CATALYTIC ACTIVITY: N deoxynucleoside triphosphate ** N diphosphate
                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa; Arthropoda; Mandibulata; Panorustacea; Hexapoda;
Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Nematocera;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01.-UNN-1994 (Rel. 29, Last sequence update)
16-027-2001 (Red. 40, Last annotation update)
Retrovirus-related Pol polyprotein from type I retrotransposable element R2 [Contains: Reverse transcriptase (EC 2.7.7.49);
                                                                                                                                                                                                                                                                                                                                                                 .;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  InterPro; IPR000477; RVTse.
Pfam; PF00078; rvt; 1.
Transferase; RNA-directed DNA polymerase; Transposable element;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NUCLEIC ACID-BINDING ENDONUCLEASE. 9584756BFA7AF818 CRC64;
                                                                 EMBL; 299113; CAB13725.1; -.
EMBL; 299114; CAB13735.1; -.
Subtlicts; BG1352; yofA.
InterPro; IPR00047; HTH_LYSR.
InterPro; IPR00119; LySR_subst.
Pfam; PF00126; HTH_1; 1.
Pfam; PF00126; HTH_1; 1.
Pfam; PF001049; HTHLYSR.
PROSITE; PS000044; HTH_LYSR_FAMILY; 1.
HYPOTHELICAL protein; Transcription regulation; DNA-binding;
                                                                                                                                                                                                                                                                                                                             Score 39; DB 1; Length 285; Pred. No. 16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    45.3%; Score 39; DB 1; Length 869; 50.0%; Pred. No. 49;
                                                                                                                                                                                                                                                                                                                                                                 5; Indels
       Usage by
                                                                                                                                                                                                                                                                   18 37 H-T-H MOTIF (POTENTIAL).
285 AA; 32050 MW; BB2E4E5D25673F73 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               REVERSE TRANSCRIPTASE.
modified and this statement is not removed. entities requires a license agreement (See hor send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                               3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Hydrolase; Nuclease; Endonuclease.
NON_TER 1 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Endonuclease] (Fragment).
Sciara coprophila (Fungus gnat).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sciaroidea; Sciaridae; Bradysia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-JUN-1994 (Rel. 29, Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 97398 MW;
                                                                                                                                                                                                                                                                                                                           45.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL; L00951; AAA29814.1; -.
                                                                                                                                                                                                                                                                                                                                                                 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                3 LNCRLYRKANKSSKL 17
                                                                                                                                                                                                                                                                                                                                                                                                                   || || : : |: || 43 ENIRLFHRTNRGMKL 57
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             009
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  869
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PIR; G44490; G44490.
                                                                                                                                                                                                                                                    Complete proteome.
DNA_BIND 18
                                                                                                                                                                                                                                                                                                                                            Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 869 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NCBI_TaxID=38358;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             <1
601
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      + {DNA}(N).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PO21_SCICO
003279;
                                                                                                                                                                                                                                                                                          SEQUENCE
                                                                                                                                                                                                                                                                                                                           Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DOMAIN
                                                                                                                                                                                                                                                                                                                                                                 Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                  g
   ŏλ
```

Best Local Similarity

```
Matches
                                                                                                                                                                                                                                                                                                                                                                            RESULT 13
                                                                                                                                                                                                                                                                                                                                  QQ
                                                                                                                                                                                                                                                                                                                                                                                                                δλ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                          STRAIN-WCS F. Serogroup B; MEDLINE-20175755; PubMed=10710307; Pettelin H., Saunders N.J., Heidelberg J., Jeffries A.C., Nelson K.E., Eisen J.A., Ketchum K.A., Hood D.W., Peden J.F., Dodson R.J., Nelson W.C., Gwinn M.L., DeBoy K., Peterson J.D., Hickey E.K., Haft D.H., Salzberg S.L., White O., Fleischmann R.D., Dougherty B.A., Hast D.H., Salzberg S.L., White O., Fleischmann R.D., Dougherty B.A., Cotton M.D., Utterback T.R., Khouri H., Qin H., Vamathevan J., Golll J., Scarlato V., Masignani V., Pizza M., Grandi G., Sun L., Snath H.O., Fraser C.M., Moxon B.R., Rappuoli R., Venter J.C.; Complete genome sequence of Nelsseria meningitidis serogroup B strain MC58.";
                                                                                                                  LBPA_NEIMB STANDARD; PRT; 943 AA.
006379; O9JTK5;
001-NOV-1995 (Rel. 32, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Lactoferrin binding protein A precursor (Iron-regulated outer membrane
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PROSITE; PS00430; TONB_DEPENDENT_REC_1; FALSE_NEG.
PROSITE; PS01156; TONB_DEPENDENT_REC_2; 1.
Outer membrane; Iron transport; Transport; TonB box; Signal; Receptor; Complete proteome.
                                                                                                                                                                                                                                                                                                                     Pettersson A., van der Ley P., Poolman J.T., Tommassen J.;
"Molecular characterization of the 98-kilodalton iron-regulated outer
                                                                                                                                                                                                                             Neisseria meningitidis (serogroup B).
Bacteria; Proteobacteria; beta subdivision; Neisseriaceae; Neisseria.
Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SCIENCE 287:1809-1815(2000).
-!- FUNCTION: UNKNOWN. MAY BE AN IRON-SIDEROPHORE RECEPTOR.
-!- SUBCELLULAR LOCATION: Outer membrane.
-!- INDUCTION: BY IRON STARVATION.
-!- SIMILARITY: LOCAL TO OTHER TONB-DEPENDENT RECEPTOR PROTEINS.
.;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LACTOFFERIN BINDING PROTEIN A.
TONB C. TERRAINAL BOX.
P -> Q (IN REF. 1).
IAT -> VAA (IN REF. 1).
A -> S (IN REF. 1).
QAGGAT -> NPETAA (IN REF. 1).
I -> V (IN REF. 1).
Indels
9
                                                                                                                                                                                                                                                                                                                                                membrane protein of Neisseria meningitidis.";
Infect. Immun. 61:4724-4733(1993).
2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               POTENTIAL
                                                                                                                                                                                                                                                                                             STRAIN=BNCV / Serogroup B;
MEDLINE=94011384; PubMed=8406871;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             InterPro; IPR000531; TonB_boxC. Pfam; PF00593; TonB_boxC; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL; AE002504; AAF41895:1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL; X69214; CAA49148.1; -.
                                                  595 AVLNCQLYASISHSCK 610
8; Conservative
                          1 AKLNCRLYRKANKSSK 16
                                                                                                                                                                                                               LBPA OR IROA OR NMB1540.
                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                       NCBI_TaxID=491;
                                                                                                                                                                                                  protein A).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CONFLICT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CONFLICT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CONFLICT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CHAIN
                                                                                                         LBPA_NEIMB
 Matches
                                                                                                                                  ò
                                                     a
```

```
This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@lsb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                        ô
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Outer membrane; Iron transport; Transport; TonB box; Signal; Receptor; Complete proteome.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Parkhill J., Achtman M., James K.D., Bentley S.D., Churcher C., Klee S.R., Morelli G., Basham D., Brown D., Chillingworth T., Davies R.M., Davis P., Devlin K., Feltwell T., Hamlin N., Holroyd S., Jagels K., Leather S., Moule S., Mungall K., Quail M.A., Rutherford K.M., Simmonds M., Skelton J., Whitehead S., Spratt B.G., Barrell B.G., Complete DNA sequence of a serogroup A strain of Neisseria
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Neisseria meningitidis (serogroup A).
Bacteria; Proteobacteria; beta subdivision; Neisseriaceae; Neisseria.
NCBL_TaxID=65699;
                                     E -> A (IN REF. I).
D -> N (IN REF. I).
DIKRKTREPFFSV -> GIKKPSEGGEYFLA (IN REF.
                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -!- FUNCTION: UNKNOWN, MAY BE AN IRON-SIDEROPHORE RECEPTOR.
-!- SUBCELLULAR LOCATION: Outer membrane.
-!- SIMILARITY: LOCAL TO OTHER TONB-DEPENDENT RECEPTOR PROTEINS.
                                                                                                                                                                                                                                                                                           -> YSDYTDKG (IN REF. 1).
                                                                                                                                                                                                                                                                                                                                                                                                                                        ;
0
                                                                                                                                                                                                                                                                                                                                                                                               DB 1; Length 943;
                                                                                                                                                                                                                                                                                                                                                                                                                                           5; Indels
                                                                                                                                                                                                                                                                                                                                                        BD569ECACFC01A84 CRC64;
                                                                                                                                                            YGK -> NGN (IN REF. 1).

Q -> M (IN REF. 1).

E -> K (IN REF. 1).

KULV -> OKLI (IN REF. 1).

A -> K (IN REF. 1).

K -> N (IN REF. 1).
                                                                                                                                                                                                                                  (IN REF. 1).
                                                                                                          (IN REF. 1).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Pfam; PF00593; TONB_DOXC; 1.
PROSITE; PS00430; TONB_DEPENDENT_REC_1; FALSE_NEG.
PROSITE; PS01156; TONB_DEPENDENT_REC_2; 1.
                                                                                                                                                                                                                                                                                                              -> V (IN REF. 1)
-> L (IN REF. 1)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       16-0cr-2001 (Rel. 40, Created)
16-0cr-2001 (Rel. 40, Last sequence update)
15-10N-2002 (Rel. 41, Last annotation update)
Lactoferrin binding protein A precursor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  944 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                           3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                     53;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STRAIN=22491 / Serogroup A / Serotype 4A;
MEDLINE-20222556; PubMed-10761919;
V -> A (IN F
R -> H (IN F
                                                                                                                                                                                                                                                                                                                                                                                                 Score 39;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      POTENTIAL.
                                                                                                                                                                                                                                                                                             STGFDENNO
                                                                                                                                                                                                                                                                                                                                                                                                                     Pred. No.
                                                                                                                                               L -> V (YGK -> N
                                                                                                          1).
RES ->
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            InterPro; IPR000531; TonB_boxC.
                                                                                                                                                                                                                                                                                                                                                            105680 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL; AL162757; CAB84967.1; -
                                                                                                                                                                                                                                                                                                                                                                                                 45.38;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        meningitidis 22491.";
Nature 404:502-506(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                           7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         481 KLNCAVYPAVDKSCR 495
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2 KLNCRLYRKANKSSK 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      27
                                                                                                                                               2281
3313
3389
3423
3455
572
658
                                                                                                                                                                                                                                                                         546
564
658
667
943 AA;
                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LBPA OR NMA1739
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LBPA_NEIMA
Q9JTK4;
                                                                                                                                                                                           CONFLICT
                                                                                                                                                                                                                                  CONFLICT
                                                                                                                                                                                                                                                                                                                   CONFLICT
  CONFLICT
                                           CONFLICT
                                                                                                                                                                                                                                                                                                                                                          SEQUENCE
                                                                                                                                                                                                                                                                              CONFLICT
                                                                                    CONFLICT
                                                                                                                              CONFLICT
                                                                                                                                                                       CONFLICT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LBPA_NEIMA
```

```
This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EWBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                    .;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                         TISSUE-Salivary gland;

TISSUE-Salivary gland;

MEDLINE-90172404; PubMed=1689777;

Paulsson G., Lendahl U., Galli J., Ericsson C., Wieslander L.;

The Balbiani ring 3 gene in Chironomus tentans has a diverged

Trepetitive structure split by many introns.";

The Balbiani ring 3 gene in Chironomus tentans has a diverged

Trepetitive structure split by many introns.";

J. Mol. Biol. 211:331-349(1990).

T. FUNCTION: USED BY THE LARVAE TO CONSTRUCT A SUPRAMOLECULAR

STRUCTORR, THE LARVAEL TUBE. Balbiani INOR PROPIEINS

TOLE AS A TRANSPORT PROTEIN THAT BINDS TO OTHER PROTEINS

INTRACELULARLY AND IN THE GLAND LUMEN IN ORDER TO PREVENT THESE

TOWN FORMING WATER INSOLUBLE FIBERS TOO EARLY.

TSSUE SPECIFICITY: SALIVARY GLAND.
                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa; Arthropoda; Mandibulata; Pancrustacea; Hexapoda;
Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Nematocera;
Chironomoidea; Chironomidae; Chironominae; Chironomus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                  0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ;
LACTOFERRIN BINDING PROTEIN A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DB 1; Length 1700;
                                                                 DB 1; Length 944;
                                                                                                  5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  21 1700 BALBIANI RING PROTEIN 3.
1700 AA; 186145 MW; 34202B28521B0815 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       4; Indels
               TONB C-TERMINAL BOX.
                                                                                                                                                                                                                                                                                           01-007-1993 (Rel. 27, Last sequence update)
16-007-2001 (Rel. 40, Last annotation update)
                                                                                                                                                                                                                                                   PRT; 1700 AA
                                                                                             3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mismatches
                                                                                 Pred. No. 53;
                                                                45.3%; Score 39; 46.7%; Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 39;
Pred. No. 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      POTENTIAL.
                                                                                                                                                                                                                                                                                                                          Balbiani ring protein 3 precursor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                InterPro; IPR004153; CXCXC_repeat. Pfam; PF03128; CXCXC; 71.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       3;
                               944 AA; 105732 MW;
                                                                                                                                                                                                                                                                            01-0CT-1993 (Rel. 27, Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; X52263; CAA36506.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      45.3%;
                                                                                                                                                                                                                                                                                                                                                                Chironomus tentans (Midge).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       53.3%;
                                                                                                7; Conservative
                                                                                                                                                               482 KLNCAVYPAVDKSCR 496
                                                                                                                                                                                                                                                  STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     8; Conservative
                                                                                                                              2 KLNCRLYRKANKSSK 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   275 AQLNCPDNKKANKET 289
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 AKLNCRLYRKANKSS 15
                                                                          Best Local Similarity
Matches 7: Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                NCBI_TaxID=7153;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Repeat; Signal.
SIGNAL
                                                                                                                                                                                                                                             BAR3_CHITE
Q03376;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    808167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE
                               SEQUENCE
                                                                Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
CHAIN
                                                                                                                                                                                                                                BAR3_CHITE
                                                                                                                                                                                                            RESULT 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Matches
FT
                                                                                                                              ōλ
                                                                                                                                                               g
                                                                                                                                                                                                                                                   ò
```

```
This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMEL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license also remement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE-92248436; PubMed-1639810; May 6.S., McGoldrick C.A., Holt C.L., Denison S.H.; May 6.S., McGoldrick C.A., Holt C.L., Denison S.H.; The bims mutation of Aspergillus nidulans uncouples DNA replication of mitosis.; J. Biol. Chem. 267:15737-15743(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ;
0
                                                                                                                              Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;
Eurotiales; Trichocomaceae; Emericella.
NCBL_TaxID=5072;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 2067;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 39; DB 1; Length zou
Pred. No. 1.2e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2067 AA; 227925 MW; E0655D939EC148DB CRC64;
                                                                                                                                                                                                                                                                                                                               MITOTIC SPINDLE.
--- SUBCELLULAR LOCATION: Nuclear.
--- SIMILARITY: TO YEAST ESPI AND S.POMBE CUTI.
                                                 Last sequence update)
PRT; 2067 AA
                                                                                                               Emericella nidulans (Aspergillus nidulans).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             3; Mismatches
                        01-077-1993 (Rel. 27, Created)
01-0CT-1993 (Rel. 27, Last sequence upc
01-FEB-1994 (Rel. 28, Last annotation u
Cell division-associated protein BIMB.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         InterPro; IPR005314; Peptidase_C50.
Pfam; PF03568; Peptidase_C50; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL; M83232; AAA33297.1; ALT_TERM.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              45.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               6; Conservative
STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Nuclear protein; Mitosis
SEQUENCE 2067 AA; 227
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PIR; A42854; A42854.
MEROPS; C50.001: -.
                                                                                                                                                                                                SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Best Local Similarity
                                                                                                                                                                                                                   STRAIN-A773;
BIMB_EMENI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Matches
```

Search completed: December 2, 2002, 10:02:51 Job time: 2.69154 secs

RESULT 15 BIMB\_EMENI

:||||:: | | 1130 RENCRIWAKVEK 1141

2 KLNCRLYRKANK 13

ŏ

		• • •

```
December 2, 2002, 10:00:15; Search time 6.08955 Seconds (without alignments) 575.215 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                                                                                                                                              671580
GenCore version 5.1.3 Copyright (c) 1993 - 2002 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                    Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                 671580 seqs, 206047115 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SUMMARIES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                            OM protein - protein search, using sw model
                                                                                                                                                                                                                                                                         BLOSUM62
Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SPTREMBL_21:*

1: sp_archea:*
2: sp_bacteria:*
3: sp_fungi:*
4: sp_human:*
5: sp_invertebrate:*
6: sp_mammal:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   sp_unclassified:*
                                                                                                                                                                                                                                    1 AKLNCRLYRKANKSSKL 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   sp_vertebrate:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             sp_mhc:*
sp_organelle:*
sp_phage:*
sp_phage:*
sp_rodent:*
sp_voirus:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        sp_rvirus:*
sp_bacteriap:*
                                                                                                                                                                                                                                                                                                                                                                                                               Minimum DB seq length: 0
Maximum DB seq length: 2000000000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 sp_archeap:*
                                                                                                                                                                                           US-09-741-106-12
86
                                                                                                                                                                                           Title:
Perfect score:
Sequence:
                                                                                                                                                                                                                                                                           Scoring table:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Database :
                                                                                                                                                                                                                                                                                                                                   Searched:
                                                                                                                 Run on:
```

	Description	O8tcel homo sapien	013815 homo sapien	091422 gallus gall	OBuvx2 sphenodon p	O8uvs2 struthio ca	OBuvs1 chelvdra se	OBuvs0 xenopus lae	O9wttl cavia porce	Ogands sus scrofa	09w648 fugu rubrip	O9pta8 salmo salar	0987s1 rhizobium 1	096171 plasmodium	O9n897 plasmodium	034413 bacillus su	Q9asw9 arabidopsis
0771177	ID	Q8TCE1	013815	091422	Q8UVX2	Q8UVS2	Q8UVS1	Q8UVS0	Q9WTT1	09GMD6	Q9W648	Q9PTA8	Q987S1	096171	768N6Q	034413	Q9ASW9
	DB	4	4	13	13	13	13	13	11	9	13	13	16	വ	Ŋ	16	10
	Query Match Length DB	259	465	423	452	453	453	456	459	169	448	452	302	2010	294	407	713
æ	Query	100.0	100.0	91.9	91.9	91.9	91.9	90.7	89.5	80.2	80.2	76.7	53.5	50.0	48.8	48.8	48.8
	Score	98	86	79	79	79	79	78	77	69	69	99	46	43	42	42	42
	Result No.	П	7	m	4.	S	9	7	8	σ	10	11	12	13	14	15	16

PRELIMINARY; PRT; 465 AA. 013815, P78439; P78447; 01-NOV-1996 (TrEMBLrel. 01, Created) 01-NOV-1996 (TrEMBLrel. 01, Last sequence update) 01-OCT-2001 (TrEMBLrel. 18, Last annotation update) Antithrombin III.

ID DT DT GN GN

OBTXAL arabidopsis O91u27 arabidopsis O91u27 arabidopsis O91u27 arabidopsis O91u27 pseudomonas O8wnm6 gorilla gor O8wnm6 porilla gor O8wnm6 porilla gor O8wnm6 perbancaarc P89686 feline immu O8wnm8 human papil O9sty9 arabidopsis O91fm8 arabidopsis O91fm8 arabidopsis O97aly covra sativ O97al clostridium O97al clostridium O97al clostridium O97al clostridium O97al drosophila O97al drosophila O9vaql drosophila O9vaql drosophila O9vbq4 drosophila	tte) ittor, clade c itta; Euteleostomi; idae; Homo.  CRC64; Length 259; Indels 0; Gaps 0;
QBRXH2 Q9LUZ7 Q9LUZ7 QBWNM6 QBWNM6 QBTRP5 QBTRP5 QBTRP5 QBVH24 Q920H4 Q92NWM8 Q91EN8 Q97EL1 Q9MBC7 Q97EL1 Q9MBC7 Q97EL1 Q9MBC7 Q97EL1 Q9MBC7 Q97EL1 Q9MBC7 Q97EL1 Q9TRS3 Q97EL1 Q9TRS9 Q9VBQ1 Q8TUM8 Q9TRS9 Q9VBQ1 Q8TUM8 Q8TUM8 Q8TUM8 Q8TUM8 Q8TUM8 Q8TUM8 Q8TUM8 Q8TUM8 Q8TUM8 Q8TUM8 Q8TUM8 Q8TUM8 Q8TUM8 Q8TUM8 Q8TUM8 Q8TUM8 Q8TUM8 Q8TUM8 Q8TUM8 Q8TUM8 Q8TUM8 Q8TUM8 Q8TUM8 Q8TUM8 Q8TUM8 Q8TUM8 Q8TUM8 Q8TUM8 Q8TUM8 Q8TUM8 Q8TUM8 Q8TUM8 Q8TUM8 Q8TUM8 Q8TUM8 Q8TUM8 Q8TUM8 Q8TUM8 Q8TUM8 Q8TUM8	ALIGNMENTS  PRT; 259 AA.  reated) st sequence update st annotation upda ) proteinase inhik  Craniata; Vertebre  Carairthini; Homini  BL/GenBank/DDBJ de  8386705A82B8EC8D  Score 86; DB 4;  Pred. No. 2.7e-07; Mismatches 0;
48.8 716 10 47.7 298 16 47.7 298 6 6 47.7 298 6 6 47.7 298 6 6 47.7 298 6 6 47.7 298 15 47.7 298 15 46.5 5 296 10 46.5 5 296 10 46.5 5 298 5 8 5 8 5 8 5 8 5 8 5 8 5 8 5 8 5 8 5	PRELIMINARY; (TrEMBLrel. (TrEMBLR) (TrEMBLR. (TrEMBLR) (Tr
118 222 222 222 222 222 222 222 233 333 33	RESULT 1  QHTCE1  DQHTCE1  AC QHTCE1  DT 01-UN-2002 (TTEMB)  DT 01-UN-2002 (TTEMB)  DT 01-UN-2002 (TTEMB)  DT 01-UN-2002 (TTEMB)  DE (antithrombin), med  DE (antithrombin), med  CS HOMO Sapiens (Human  OC HORATOGA; MATAZOA  OC Mammalia; Eutheria  NCH_TAXID=9606;  RN 61250ELIYER;  RA STRANDEFRENOM N.A.  RA STRANDEFRENOM  OUETY MATCH  DEST LOCAL SIMILATITY  MATCHES 17; CONSETT  OUETY MATCH  RESULT 2  Q13812

ó

```
q
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 δλ
                                                                                                                                                                                                  qq
                                                                                                                                                                                                                                                     á
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
Antithrombin (Fragment).
Gallus gallus (Chicken).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                   SEQUENCE OF 138-255 FROM N.A.
MEDLINE-89050967; PubMed-3191114;
Bock S.C., Marrinan J.A., Radziejewska E.;
"Antithrombin III Utah: proline-407 to leucine mutation in a highly conserved region near the inhibitor reactive site.";
Biochemistry 27:6171-6178(1988).
Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                Bock S.C., Levitan D.J.; "Characterization of an unusual DNA length polymorphism 5' to the
                                                                                                                                                                                                                                                                     Tsuji H., Takada O., Nakagawa M., Tanaka S., Hashimoto-Gotoh T.;
Submitted (NoV-1994) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         100.0%; Score 86; DB 4; Length 465; 100.0%; Pred. No. 4.8e-07;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0; Indels
                                                                                                                                                                                                                                SEQUENCE OF 1-13 FROM N.A.
Rosenberg J.B., Amrani D.L., Bergtrom G.;
Submitted (AUG-1994) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                      465 AA; 52691 MW; C69214FCA12766D0 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      423 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0; Mismatches
                                                                                                                                                                                                    human antithrombin III gene.";
Nucleic Acids Res. 11:8569-8582(1983).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-NOV-1996 (TrEMBLrel. 01, Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
MEDLINE=96114615; PubMed=7495074;
Tejada ★/L∵, Degley R.G.;
                                                                                                                                                            SEQUENCE OF 1-14 FROM N.A. MEDLINE=84169500; PubMed=6672771;
                                                                                                                                                                                                                                                                                                                                                             EMBL, D29832, BAA06212.1;
EMBL, X00238; CAA25060.1;
EMBL, X00237, CAA25059.1;
EMBL, U11270; AAA19930.1;
HSSP, P01008; ZANT
                                                                                                                                                                                                                                                                                                                                                                                                             InterPro; IPR000215; Serpin.
Pfam; PF00079; Serpin; 1.
SMART; SM00093; SERPIN; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      157 AKLNCRLYRKANKSSKL 173
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 AKLNCRLYRKANKSSKL 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity 100.
Matches 17; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRELIMINARY;
                                                  SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NCBI_TaxID=9031;
                               MCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                              Serpin; Signa
                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Q91422
Q91422;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gallus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT 3
Q91422
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     g
```

```
Gaps
                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Palaeognathae; Struthioniformes; Struthionidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sphenodon punctatus (Hatteria) (Tuatara).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Lepidosauria; Sphenodontia; Sphenodontidae; Sphenodon.
NCBI_TaxID=8508;
                                                                                                                                                                                                                                                                                                                                                                                              .;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
"Cloning of an avian antithrombin: developmental and hormonal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Metcalf V.J., Brennan S.O., George P.M., Chambers G.K.;
Metcalf V.J., Brennan S.O., George P.M., Chambers G.K.;
"The identification of liver-expressed genes from tuatara.";
Submitted (JAN-2001) to the EMBL/GenBank/DDBJ databases.
EMBL, AR335570; AAL73207.1; -.
InterPro; IPR000215; Serpin.
Pfam: PR00079; serpin: 1.
SMART; SM00093; SERPIN: 1.
SEQUENCE 452 AA; 51807 MW; 380C1C653959DA07 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           91.9%; Score 79; DB 13; Length 452; 88.2%; Pred. No. 8.2e-06; ive 2; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                        91.9%; Score 79; DB 13; Length 423; 88.2%; Pred. No. 7.7e-06; Live 2; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                             423 AA; 48128 MW; 5C559B91312D1F25 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-WAR-2002 (TrEMBLrel. 20, Last sequence update) 01-JUN-2002 (TrEMBLrel. 21, Last annotation update) Antithrombin III.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Last sequence update)
Last annotation update)
                      regulation of expression.";
Thromb. Haemost. 73:654-661(1995).
-- SIMILARITY: BELONGS TO THE SERPIN FAMILY.
-- SEMBL: S79838; AAB35653.1;
-- HSSP: P41361; LATT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRT; 453 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  452 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              QBUVS2;
01-MAR-2002 (TrEMBLrel. 20, Created)
MAR-2002 (TrEMBLrel. 20, Last seq.
01-JUN-2002 (TrEMBLrel. 21, Last anno
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-MAR-2002 (TrEMBLrel. 20, Created)
                                                                                                                                                                                                                         PROSITE; PS00284; SERPIN; UNKNOWN_1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
Backovic M., Gettins P.G.W.;
                                                                                                                                             Interpro; IPR000215; Serpin.
Pfam; PF00079; Serpin; 1.
SMART; SM00093; SERPIN; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Struthio camelus (Ostrich)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            144 AKLNCRLYKKANKSSEL 160
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          115 AKLNCRLYKKANKSSEL 131
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 AKLNCRLYRKANKSSKL 17
                                                                                                                                                                                                                                                                                                                                                                                                                                              1 AKLNCRLYRKANKSSKL 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Matches 15; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                  Local Similarity
nes 15; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NCBI_TaxID=8801;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Antithrombin.
                                                                                                                                                                                                                                                                                                   SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Struthio
                                                                                                                                                                                                                                                                                                                                                   Query Match
                                                                                                                                                                                                                                                                              NON TER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Q8UVS2
                                                                                                                                                                                                                                                       Serpin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Q8UVX2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT 5
Q8UVS2
                                                                                                                                                                                                                                                                                                                                                                                                   Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 4
QBUVX2
```

ó:

```
09GMD6
                                                                                                                                                                                                                                Q9WTT1
  RT
RE
DR DR
DR DR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 q
                                                                                                                                                                               qq
                                                                                                                                                                                                                                           δ
                                                                                                                                                         ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
Backovic M., Gettins P.G.W.;
"Insight into residues critical for antithrombin function from an expanded database of sequences that includes frog, turtle and ostrich
                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
Backovic M., Gettins P.G.W.;
"Insight into residues critical for antithrombin function from an expanded database of sequences that includes frog, turtle and ostrich
"Insight into residues critical for antithrombin function from an expanded database of sequences that includes frog, turtle and ostrich
                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                      cukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Testudines; Cryptodira; Testudinoidea; Chelydridae; Chelydrae.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Xenopus laevis (African clawed frog).
Wataryota; Metacoa; Chordata; Craniata; Vertebrata; Euteleostomi; Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae; Xenopodinae; Xenopus.
                                                                                                                                                         ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0;
                                                                                                                                 Length 453;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 453;
                     antithrombins.";
Submitted (AUG-201) to the EMBL/GenBank/DDBJ databases.
EMBL, AR16011. AAL60465.1;
InterPro; 118010.215; Serpin.
Pfam; PF00079; Serpin; 1.
SMART; SM00093; SERPIN; 1.
PROSITE, PS00284; SERPIN; UNKNOWN_1.
SROUENCE 453 AA; 51403 MW; 4283370BF0C6CFFF CRC64;
                                                                                                                                                        Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Submitted (AUG-2001) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                BUBL; AF411692; AALG0466.1; -
InterPro: IPR000215; Serpin.
Pfam; PR00079; SerpIn; 1.
PROSITE; PS00284; SERPIN; UNKNOWN_1.
SEQUENCE 453 AA; 51593 MW; A86A8ABC7798799E CRC64;
                                                                                                                                                                                                                                                                                     01-MAR-2002 (TrEMBLrel. 20, Created)
01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-WAR-2002 (TrEMBLrel. 20, Created)
01-WAR-2002 (TrEMBLrel. 20, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     91.9%; Score 79; DB 13; L
88.2%; Pred. No. 8.2e-06;
tive 2; Mismatches 0;
                                                                                                                               91.9%; Score 79; DB 13; L
88.2%; Pred. No. 8.2e-06;
tive 2; Mismatches 0;
                                                                                                                                                                                                                                                                453 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        456 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRT;
                                                                                                                                                                                                                                                                PRT;
                                                                                                                                                                                          145 AKLNCRLYKKANKSSEL 161
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   145 AKLNCRLYKKANKSSEL 161
                                                                                                                                                                              1 AKLNCRLYRKANKSSKL 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 AKLNCRLYRKANKSSKL 17
                                                                                                                                           Best_Local Similarity 88.2
Matches 15; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Best Local Similarity 88.2
Matches 15; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRELIMINARY;
                                                                                                                                                                                                                                                                PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                               antithrombins."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NCBI_TaxID=8355
                                                                                                                                                                                                                                                                                                                          Antithrombin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Antithrombin.
                                                                                                                                Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
                                                                                                                                                                                                                                                                           08UVS1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Q8UVSO;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Q8UVS0
                                                                                                                                                                                                                                                               Q8UVS1
                                                                                                                                                                                                                                         RESULT 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Q8UVS0
                                                                                                                                                                                                                                                    Q8UVS1
 δλ
                                                                                                                                                                                                                                                                           δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            g
```

```
Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Cavia porcellus (Guinea pig).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Hystricognathi; Caviidae; Cavia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sus scrofa (Pig).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ;
0
                                                                                                                                                                                                                                                        ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 459;
                                                                                                                                                                                                          Length 456;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        89.5%; Score 77; DB 11; Length 45
100.0%; Pred. No. 1.9e-05;
Live 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                      Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Schuetz E., Andag R., Wieland E.;
"Landrace pig Antithrombin 3, partial cDNA.";
Submitted (JUN-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          "Guinea pig gene for antithrombin III.";
Submitted (MAY-1999) to the EMBL/GenBank/DDBJ databases.
-i- SINLLARITY: BELONGS TO THE SERPIN FAMILY.
EMBL; AB027233; BAA77781.1; -.
HSSP; PO1008; 1ATH.
              Submitted (NGG-2001) to the EMBL/GenBank/DDBJ databases. EMBL, AF411693, AAL60467.1; -. InterPro: JPR00215; Serpin. Pfam: PF000915; Serpin. Samar; SM00093; Serpin: 1. PROSITE; PS00294; SERPIN: 1. SEQUENCE 456 AA: 51851 MW: 03E086F3ABCEA85C CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 459 AA; 51912 MW; B1E36FB732592824 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-NOV-1999 (TrEMBLrel. 12, Created)
01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-WAR-2001 (TrEMBLrel. 16, Created)
01-WAR-2001 (TrEMBLrel. 16, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
                                                                                                                                                                                  90.7%; Score 78; DB 13; L
88.2%; Pred. No. 1.2e-05;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     459 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         169 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PROSITE; PS00284; SERPIN; UNKNOWN_1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      HSSP; P01008; 1ATH.
InterPro; IPR000215; Serpin.
Pfam; PF00079; serpin; 1.
SMART; SM00093; SERPIN; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Antithrombin III (Fragment)
                                                                                                                                                                                                                                                                                                                             147 AKINCRLFRKANKSSEL 163
                                                                                                                                                                                                                                                                                                       1 AKLNCRLYRKANKSSKL 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            15; Conservative
                                                                                                                                                                                                                                                        Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  151 AKLNCRLYRKANKSS 165
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 AKLNCRLYRKANKSS 15
                                                                                                                                                                                                                           Best_Local Similarity
Matches 15; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NCBI_TaxID=10141;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Antithrombin III.
antithrombins.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NCBI_TaxID=9823;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TISSUE-LIVER;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Suzuki Y.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE
                                                                                                                                                                                                            Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Q9WTT1
Q9WTT1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Q9GMD6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Q9GMD6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Matches
                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 9
```

```
;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ·.
                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-NOV-1999 (TrEMBLrel. 12, Created)
01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
Antithrombin III.
Fugu rubripes (Japanese pufferfish) (Takifugu rubripes).
Bugaryota: Metzaca, Chordata; Craniata; Vertebrata; Euteleostomi; Actinopterygii; Neopterygii; Teleostei; Buteleostei; Neoteleostei; Acanthomorpha; Acanthomorpha; Acanthomorpha; Acanthomorpha; Tetraodontidae; Takifugu.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Antithrombin precursor.

ANTITHROMBIN.
Salmo salar (Atlantic salmon).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Euteleostei;
Protacanthopterygii; Salmoniformes; Salmonidae; Salmo.

NCBI_TaxID-8030;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.

MEDLINRE-20177689; PubMed=10712595;
Andersen O., Flengsrud R., Norberg K., Salte R.;
"Salmon-entithrombin has only three carbohydrate side chains, and
                                                                                                                                                                                                                                                                                         .;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                .;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             80.2%; Score 69; DB 13; Length 448; 76.5%; Pred. No. 0.00048; ive 3; Mismatches 1; Indels
                                                                                                                                                                                                                         80.2%; Score 69; DB 6; Length 169; 100.0%; Pred. No. 0.00019;
                                                                                                                                                                                                                                                                                  0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           "Pufferfish gene for antithrombin III.";
Submitted (APR-1999) to the EMBL/GenBank/DDBJ databases.
-i- SHILLARITY: BELONGS TO THE SERPIN FAMILY.
EMBL; ABO26832; BAA77461.1; -.
HSSP; PO1008; 1ATH.
EMBL; AF281653; AAG01450.1; -.
HSSP; P41361; 1ATT.
InterPro; IPR000215; Serpin.
PGAM: PF00079; Serpin; 1.
NON_TER 169 169
SEQUENCE 169 AA; 19170 MW; 182B1BC2D1C11A21 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       448 AA; 50585 MW; A9037E2FCD59D3FE CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-WAY-2000 (TrEMBLrel. 13, Created)
01-WAY-2000 (TrEMBLrel. 13, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     448 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         452 AA.
                                                                                                                                                                                                                                         100.0%; Pred. nc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              InterPro; IPR000215; Serpin.
Pfam: PF00079; serpin; 1.
SRMRT: SM00093; SERPIN; 1.
PROSITE; PS00284; SERPIN; UNKNOWN_1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 AKLNCRLYRKANKSSKL 17
                                                                                                                                                                                                                                                     Best Local Similarity 100.
Matches 13; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Best Local Similarity 76.5
Matches 13; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                     157 AKLNCRLYRKANK 169
                                                                                                                                                                                                                                                                                                                                                  1 AKLNCRLYRKANK 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NCBI_TaxID=31033;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE
                                                                                                                                                                                                                         Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               09W648;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Q9W648
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Q9PTA8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 10
Q9W648
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 11
Q9PTA8
                                                                                                                                                                                                                                                                                                                                                                                                        Db
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A PAC 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ó
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DR DR SS FT SS
                                                                                                                                                                                                                                                                                                                                                     ò
```

```
Kaneko T., Nakamura Y., Sato S., Asamizu E., Kato T., Sasamoto S., Watanabe A., Idesawa K., Ishikawa A., Kawashima K., Kimura T., Kiyokawa C., Kohara M., Matsumoto M., Matsuno A., Mochizuki Y., Nakayama S., Nakazaki N., Shimpo S., Sugimoto M., Takeuchi C., Yamada M., Tabata S., Nakayama S., Complete genome structure of the nitrogen-fixing symbiotic bacterium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Rhizobium loti (Mesorhizobium loti).
Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group;
Phyllobacteriaceae; Mesorhizobium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
                                                                                                                                                                                                                                                                                                                                                                                                              76.7%; Score 66; DB 13; Length 452; 70.6%; Pred. No. 0.0017; Live 4; Mismatches 1; Indels
shows functional similarities to human beta-antithrombin.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 302;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 4; Indels
                                                                                                                                                                                                                                                                                                                              ANTITHROMBIN.
797568B0727B46E8 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                302 AA; 32873 MW; 630BE56B26FEC4D5 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  096751;
01-OCT-2001 (TrEMBLrel. 18, Created)
01-OCT-2001 (TrEMBLrel. 18, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-MAY-1999 (TrEMBLrel. 10, Created)
01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       53.5%; Score 46; DB 16; 43.8%; Pred. No. 3.9;
                     EUT. J. BIOChem. 267:1651-1657(2000).
-!- SIMILARITY: BELONGS TO THE SERPIN FAMILY.
EMBL, AJ552153, CAB64714.1; -.
Interpro; IPRO00215; Serpin.
Pf00079; Serpin.
PRO0079; Serpin.
PROSTITE; PSO0284; SERPIN; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Pfam; PF00126; HTH_1; 1.
Pfam; PF03466; LysR_substrate; 1.
PRINTS; PR00039; HTHLYSR.
Complete proteome.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             302 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRT; 2010 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 5; Mismatches
                                                                                                                                                                                                                                                                                                   POTENTIAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STRAIN-MAFF303099;
MEDLINE=21082930; PubMed=11214968;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mesorhizobium loti.";
DNA Res. 7:331-338(2000).
EMBL; AP003010; BAB53129.1; -.
INTERPRO; IPR000847; HTH LysR.
InterPro; IPR005119; LysR_subst.
                                                                                                                                                                                                                                                                                                1 22 PC
23 452 AI
452 AA; 51471 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 AKLNCRLYRKANKSSKL 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                Best_Local Similarity 70.6
Matches 12; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Best_Local Similarity 43.8
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          :|||||: : || :: 45 RENCRLFERGGKSVRM 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2 KLNCRLYRKANKSSKL 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                 Serpin; Signal.
SIGNAL 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NCBI_TaxID=381;
                                                                                                                                                                                                                                                                                                                                                          SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MLL6938
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              096171;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   096171
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                098781
                                                                                                                                                                                                                                                                                                                                 CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 12
Q987S1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT 13
096171
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AC AC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                qq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ACCOORDING TO THE PROPERTY OF 
   RT CCC CC DR PTT FTT SO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            δλ
```

ó

```
ő
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ;
0
                                                                                                          MEDITRE 99021743; PubMed-9804551;
Gardner M.J., Tettelin H., Carucci D.J., Cummings L.M., Aravind L.,
Koonin E.V., Shallom S., Mason T., Yu K., Fujii C., Pederson J.,
Shen K., Jing J., Aston C., Lai Z., Schwartz D.C., Pertea M.,
Salzberg S., Zhou L., Sutton G.G., Clayton R., White O., Smith H.O.,
Fraser C.M., Adams M.D., Venter J.C., Hoffman S.L.;
"Chromosome 2 sequence of the human malaria parasite Plasmodium
                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Oliver K., Bowman S., Hall N., Quail M., Rajandream M.A., Harris D., del Portillo H.A., Lanzer M., Barrell B.G.; Submitted (JUN-2000) to the EMBL/GenBank/DDBJ databases. EMBL, AL360354; CAB96698 I, - SEQUENCE 294 AA; 34499 MW; 54F05C523996ED57 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ;
0
                                                                                                                                                                                                                                                                                                                                                  0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Bacteria; Firmicutes; Bacillus/Clostridium group; Bacillales;
                                                       Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
NCBL_TaxID=5833;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium
NCBI_TaxID=5855;
                                                                                                                                                                                                                                                                                                                    DB 5; Length 2010; 85;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 294;
                                                                                                                                                                                                                                           EMBL, AE001391; AAC71865.1; -.
InterPro; IPR001064; Crystallin.
PROSITE; PS00225; CRYSTALLIN_BETAGAMMA; UNKNOWN_1.
SEQUENCE 2010 AA; 241791 MW; 6E30760AB70AAZF3 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           4; Indels
                                                                                                                                                                                                                                                                                                                                                 4; Indels
01-JUN-2001 (TrEMBLrel. 17, Last annotation update) Phosphatase (acid phosphatase family).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 42; DB 5;
Pred. No. 20;
3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 294 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        407 AA.
                                                                                                                                                                                                                                                                                                                                                 Mismatches
                                                                                                                                                                                                                                                                                                                    Score 43;
Pred. No. 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRT;
                                                                                                                                                                                                                                                                                                                    50.0%;
57.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              48.8%;
                                                                                                                                                                                                                 falciparum.";
Science 282:1126-1132(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-OCT-2000 (TrEMBLrel. 15, 01-OCT-2000 (TrEMBLrel. 15, 01-OCT-2000 (TrEMBLrel. 15,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-JAN-1998 (TrEMBLrel. 05, 01-JAN-1998 (TrEMBLrel. 05, 01-MAR-2002 (TrEMBLrel. 20,
                                                                                                                                                                                                                                                                                                                                                 Conservative
                                                                                                                                                                                                                                                                                                                                                                                              : | | | | | | : |
1359 INVRLYEKYNKENK 1372
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      |: |:||| || :
248 LSLRMYRKKNKYSNI 262
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    3 LNCRLYRKANKSSKL 17
                                                                                                                                                                                                                                                                                                                                                                              3 LNCRLYRKANKSSK 16
                                          Plasmodium falciparum.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Bacillaceae; Bacillus.
                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity
                                                                                    [1]
SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Bacillus subtilis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Plasmodium vivax.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NCBI_TaxID=1423;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Vir9 protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               09N897;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       034413;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                09N897
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        034413
                                                                                                                                                                                                                                                                                                                                                 Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                YTCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Q9N897
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         034413
                                                                                                                                                                                                                                                                                                                                                                                                       Dp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      δλ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                g
```

```
RA Kunst F., Ogasawara N., Moszer I., Albertini A.M., Alloni G.,
RA Kunst F., Ogasawara N., Moszer I., Albertini A.M., Alloni G.,
RA Azevedo V., Bertero M.G., Bessieres P., Bolotin A., Borchert S.,
RA Brouillet S., Bruschi C.V., Caldwell B., Capuano V., Carter N.M.,
RA Brouillet S., Bruschi C.V., Caldwell B., Capuano V., Carter N.M.,
RA Brouillet S., Daviner K.M., Dusterhoft A., Erlich S.D., Emmerson P.T.,
RA Britz C., Fujita M., Fujita Y., Fuma S., Galizzi A., Galleron N.,
RA Entian K.D., Errington J., Febret C., Ferrari E., Foulger D.,
RA Guiseppi G., Guy B.J., Haga K., Haicoh J., Harwood C.R., Henaut A.,
RA Hilbert H., Holsappel S., Hosono S., Hullo M.F., Itaya M., Jones L.,
RA Kuriata D., Kasahara Y., Klaerr-Blanchard M., Klein C.,
RA Kurita K., Lapidus A., Liu H., Masuda S., Mauel C., Medigue C.,
RA Modina N., Mellado R.P., Koningstein G., Krogh S., Kumano M.,
RA Noone D., O'Reilly M., Ogawa K., Ogiwara A., Oudega B., Park S.H.,
RA Presecan E., Pujic P., Purnelle B., Rapoport G., Rey M., Sadaie Y.,
RA Berson E., Pujic P., Purnelle B., Rapoport G., Rey M., Sadaie Y.,
RA Sekiguchi J., Sekwaka A., Seror S.J., Serror P., Shin B.S., Soldo B.,
RA Sekiguchi J., Sekwaka A., Seror S.J., Serror P., Shin B.S., Soldo B.,
RA Seto T., Scanlan E., Schleich S., Schroeter R., Scoffone F.,
RA Tosacovi A., Tanaka T., Tarakanshi H., Takemaru K.,
RA Tosacovi B., Wadler E., Wedler E., Wedler H., Weitzenegger T.,
RA Tosacovi W., Uchiyama S., Vandenbol M., Vannier F., Vassarotti A.,
RA Winters P., Wipat A., Yamamoto H., Yamane K., Yasumoto K., Yata K.,
RY Shillswaw H.F., Zumstein E., Yoshikawa H., Danchin A.;
Ry Shillswaw H.F., Zumstein E., Yoshikawa H., Danchin A.;
Ry Sathillswaw H.F., Zumstein E., Yoshikawa H., Danchin A.,
Ry Sathillswaw H.F., Zumstein E., Yoshikawa H., Danchin A.,
Ry Sathillswaw H.F., Zumstein E., Yoshikawa H., Danchin A.,
Ry Sathillswaw H.F., Zumstein E., Yoshikawa H., Danchin A.,
Ry Sathillswaw H.F., Zumstein E., Yoshikawa H., Danchin A.,
Ry Sathillswaw H.F., Zumstein E., Yoshikawa H., Danchin A.,
Ry Sathill
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 48.8%; Score 42; DB 16; Length 407; 53.3%; Pred. No. 27;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels
                                              Lapidus A., Galleron N., Sorokin A., Ehrlich D.; Submitted (JUN-1997) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Kunst F., Ogasawara N., Yoshikawa H., Danchin A.;
Submitted (NOV-1997) to the EMBL/GenBank/DDBJ databases.
EMBL; AF008220; AAC000555.1; -.
EMBL; 29919; CAB15066.1; -.
InterPro; IPR001296; Glycos_transf_1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   407 AA; 46160 MW; BB6C767461A136D2 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Pred. No. 27;
4; Mismatches
                                                                                                                                                                   MEDLINE=98044033; PubMed=9384377;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           53.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Nature 390:249-256(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                3 LNCRLYRKANKSSKL 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Local Similarity
nes 8; Conserv
                       SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
                                                                                                                     SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Complete proteome. SEQUENCE 407 AA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRAIN=168;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Matches
Óλ
```

Search completed: December 2, 2002, 10:04:12 Job time: 8.08955 secs

90 LNVSLYKKASPNSKI 104

g

			•
			•
			k'
			•